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**United States Patent** [19]**Kubota et al.**[11] **Patent Number:** **5,830,715**[45] **Date of Patent:** **\*Nov. 3, 1998**[54] **DNA ENCODING ENZYME, RECOMBINANT DNA AND ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES**[75] Inventors: **Michio Kubota**, Osaka; **Keiji Tsusaki**, Okayama; **Kazuko Hattori**, Okayama; **Toshiyuki Sugimoto**, Okayama, all of Japan[73] Assignee: **Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo**, Okayama, Japan

[\*] Notice: The term of this patent shall not extend beyond the expiration date of Pat. No. 5,716,813.

[21] Appl. No.: **961,240**[22] Filed: **Oct. 30, 1997****Related U.S. Application Data**

[60] Continuation of Ser. No. 607,321, Feb. 26, 1996, Pat. No. 5,716,813, which is a division of Ser. No. 399,646, Mar. 7, 1995, Pat. No. 5,556,781.

[30] **Foreign Application Priority Data**Mar. 7, 1994 [JP] Japan ..... 6-59834  
Mar. 7, 1994 [JP] Japan ..... 6-59840[51] **Int. Cl.<sup>6</sup>** ..... **C12N 9/24**; C12N 9/26; C12N 1/02; C13J 1/00[52] **U.S. Cl.** ..... **435/96**; 435/200; 435/201; 435/276[58] **Field of Search** ..... 435/96, 200, 201, 435/276[56] **References Cited****U.S. PATENT DOCUMENTS**4,521,252 6/1985 Miyake et al. .... 127/46.3  
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5,472,863 12/1995 Maruta et al. .... 435/200**FOREIGN PATENT DOCUMENTS**0555540 12/1992 European Pat. Off. .  
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2106912 4/1983 United Kingdom .**OTHER PUBLICATIONS**E.M. Southern *Detection of Specific Sequences Among DNA Fragments Separated by Gel Electrophoresis*, J. Mol. Biol., vol. 98, pp. 503–517, 1975.*Enzyme Kinetics of Amylases and Related Enzymes*, Handbook of Amylases and Related Enzymes, pp. 1–9, 1988.Maruta et al., *Biochimica et Biophysica Acta*, “Cloning and Sequencing of Trehalose Biosynthesis Genes from *Arthrobacter* sp. Q36”, No. 1289, 1996, pp. 10–13.U.K. Laemmli, *Cleavage of Structural Proteins During the Assembly of the Head of Bacteriophage T4*, *Nature*, vol. 227, pp. 680–685, 15 Aug. 1970.J. Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Edition, published by Cold Spring Harbor Laboratory Press, 1989, pp. 9.47–9.58 and 11.45–11.54.*Primary Examiner*—Eric Grimes*Assistant Examiner*—Lisa J. Hobbs*Attorney, Agent, or Firm*—Browdy and Neimark[57] **ABSTRACT**

Disclosed are a DNA encoding an enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, recombinant DNA and enzyme, transformant, and their preparations and uses. These facilitate the industrial-scale production of trehalose with a relative easiness and low cost, and trehalose thus obtained can be satisfactorily used in a variety of food products, cosmetics and pharmaceuticals.

**7 Claims, 9 Drawing Sheets**

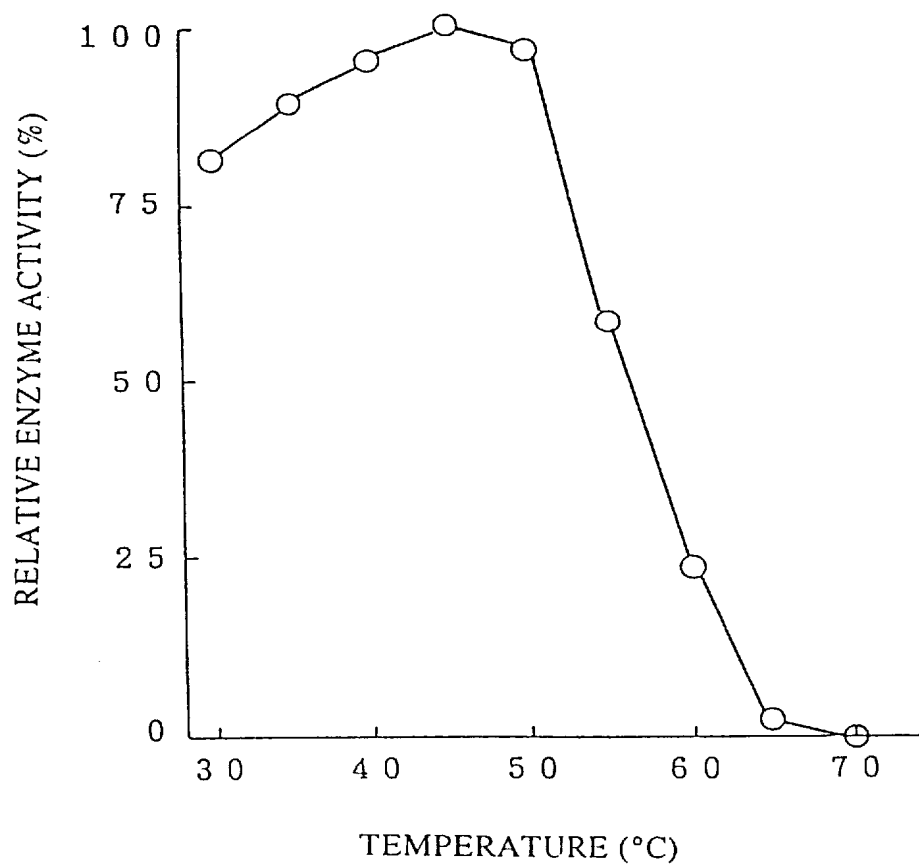


FIG. 1

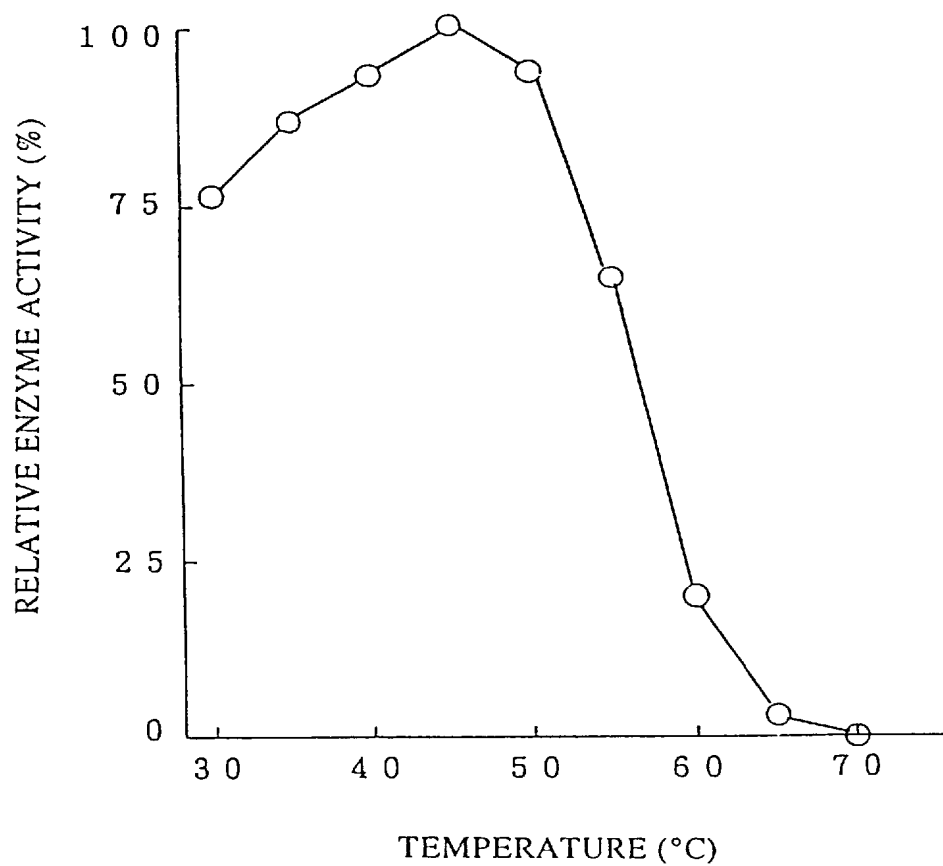


FIG. 2

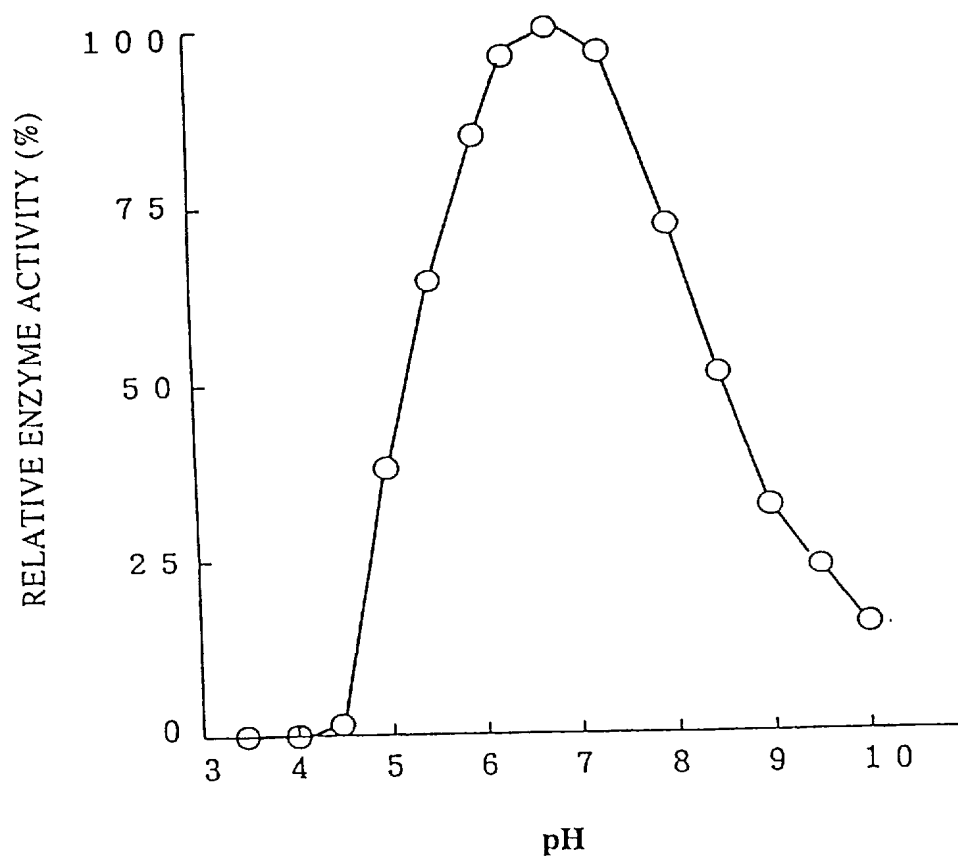


FIG. 3

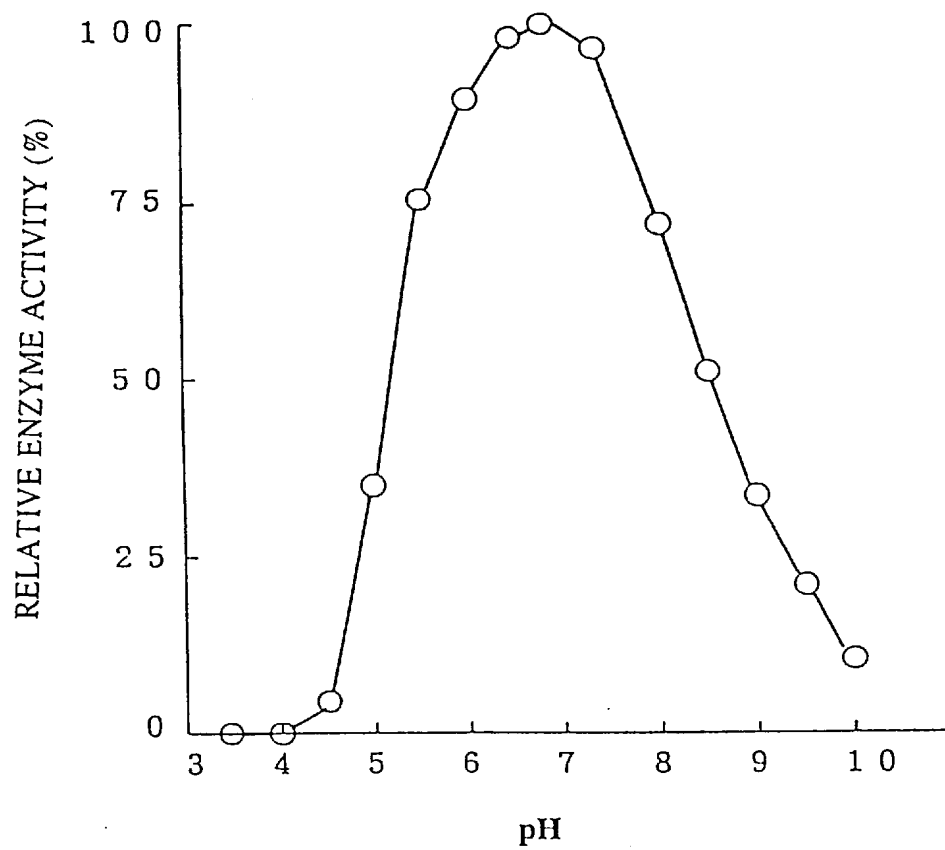


FIG. 4

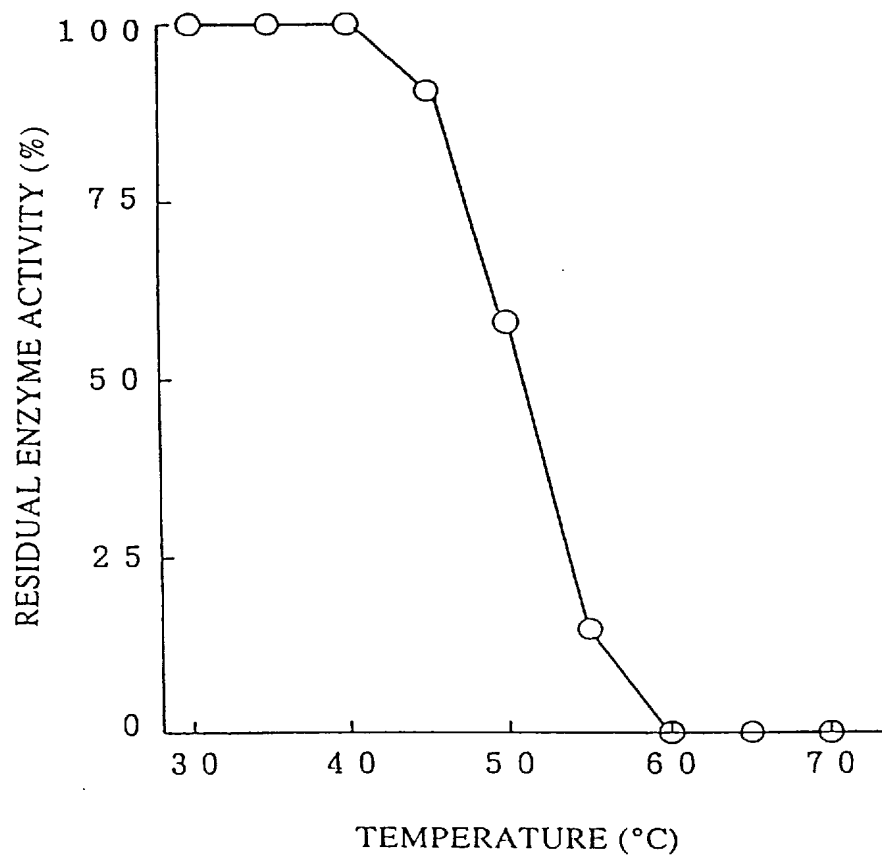


FIG. 5

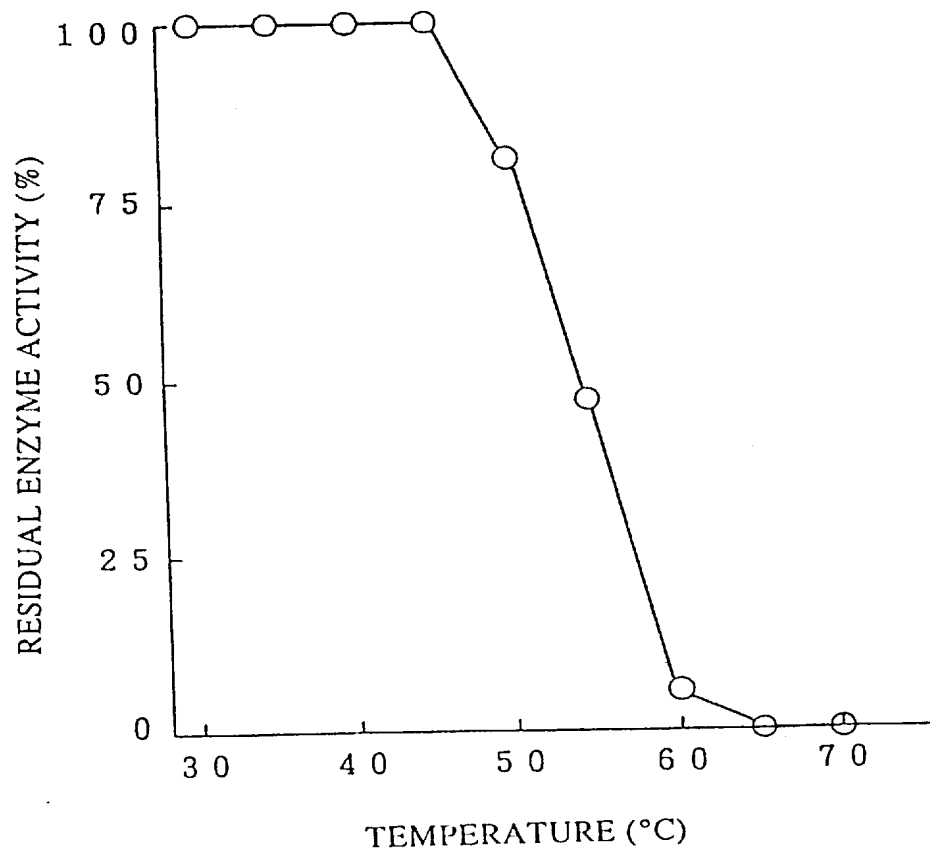


FIG. 6

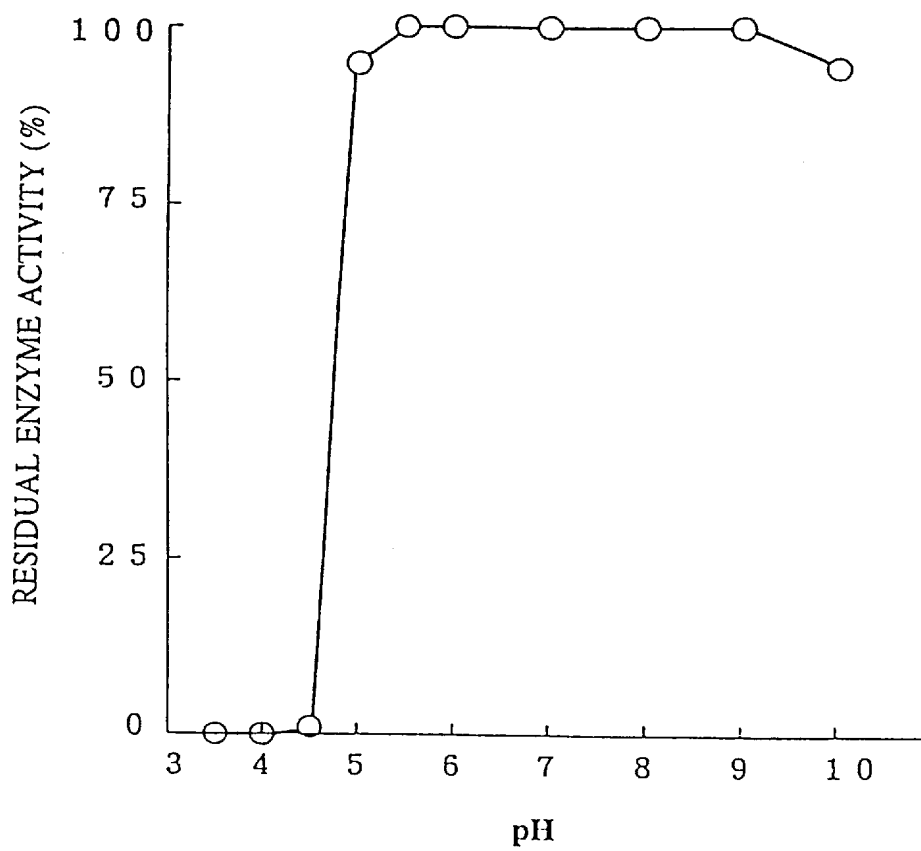


FIG. 7



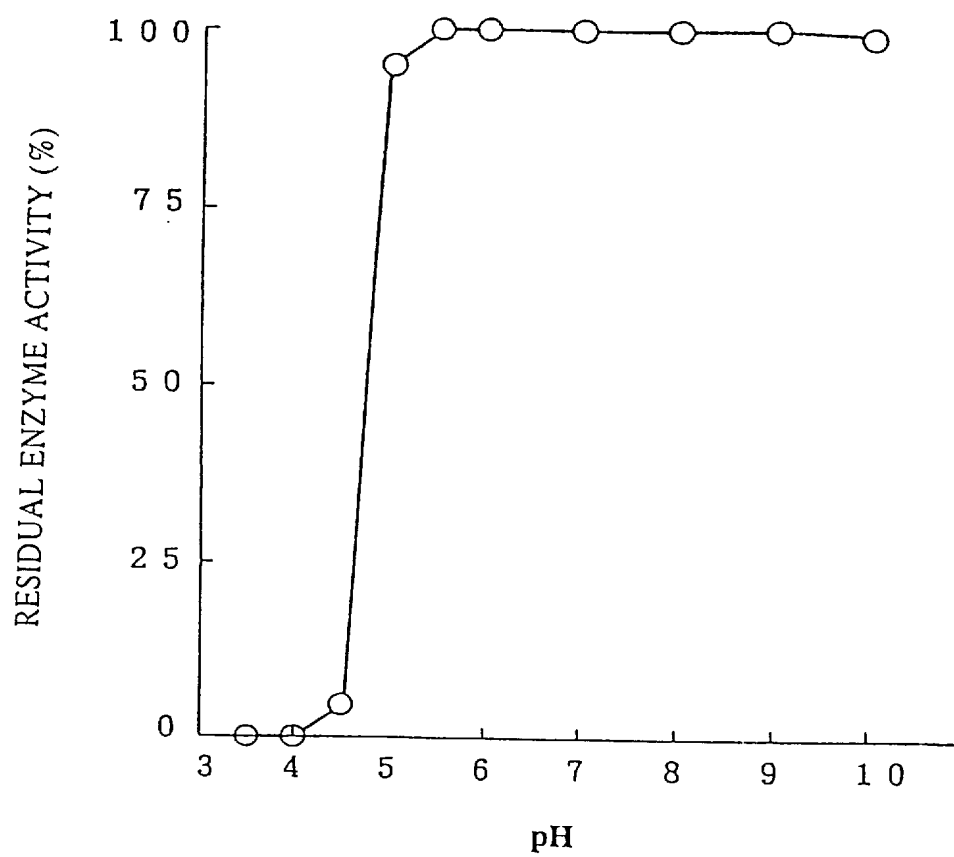


FIG. 8

FIG. 9

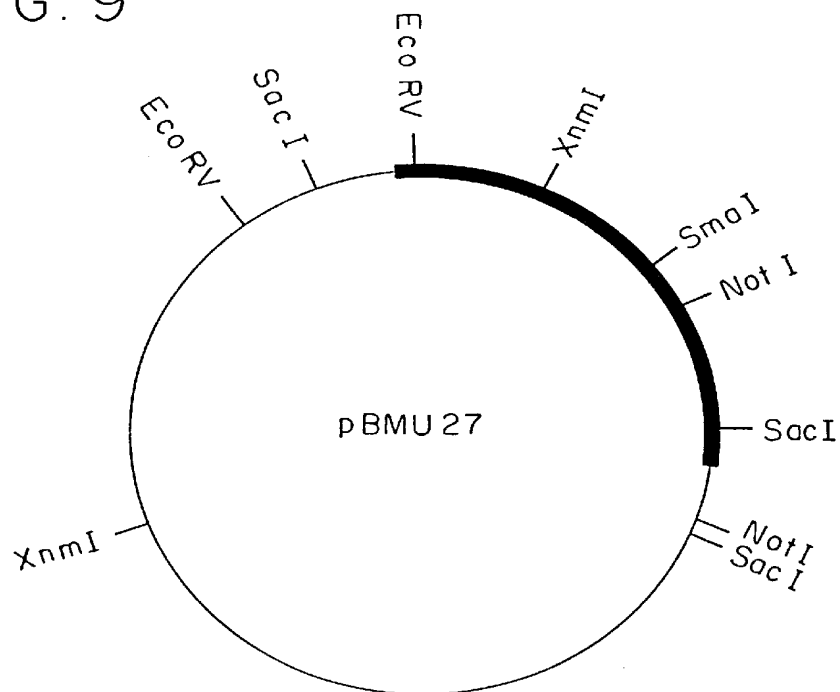
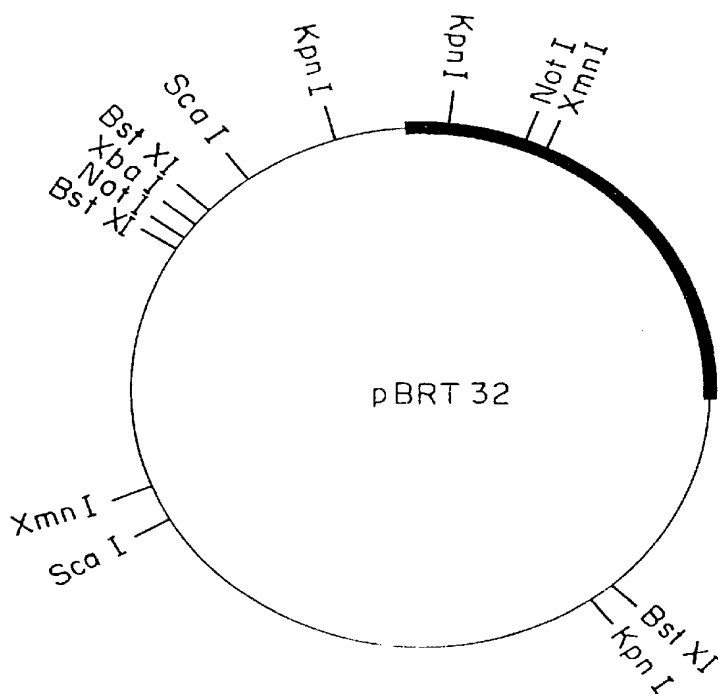


FIG. 10



# **DNA ENCODING ENZYME, RECOMBINANT DNA AND ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USES**

This is a continuation of parent application Ser. No. 08/607,321 filed Feb. 26, 1996, now issued as U.S. Pat. No. 5,716,813, which is a divisional of application Ser. No. 08/399,646, filed Mar. 7, 1995, now issued as U.S. Pat. No. 5,556,781.

## **BACKGROUND OF THE INVENTION**

### **1. Field Of The Invention**

The present invention relates to a novel DNA encoding an enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, recombinant DNA containing the same, and a transformant, and further relates to a recombinant enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, as well as to preparations and uses thereof.

### **2. Description Of The Prior Art**

Trehalose is a disaccharide which consists of 2 glucose molecules which are linked together with their reducing groups, and, naturally, it is present in bacteria, fungi, algae, insects, etc., in an extremely small quantity. Having no reducing residue within the molecule, trehalose does not cause an unsatisfactory browning reaction even when heated in the presence of amino acids or the like, and because of this it can sweeten food products without fear of causing unsatisfactory coloration and deterioration. Trehalose, however, is far from being readily prepared in a desired amount by conventional methods, and, actually, it has not scarcely been used for sweetening food products.

Conventional methods are roughly classified into 2 groups, i.e. the one using cells of microorganisms and the other employing a multi-enzymatic system wherein enzymes are allowed to act on saccharides. The former, as disclosed in Japanese Patent Laid-Open No.154,485/75, is a method which comprises allowing to grow microorganisms such as bacteria and yeasts in a nutrient culture medium, and collecting trehalose from the proliferated cells in the resultant culture. The latter, as disclosed in Japanese Patent Laid-Open No.216,695/83, is a method which comprises providing maltose as a substrate, allowing a multi-enzymatic system using maltose- and trehalose-phosphorylases to act on maltose, and isolating the formed trehalose from the reaction system. Although the former facilitates the growth of microorganisms with a relative easiness, it requires a sequentially-complicated step for collecting trehalose from the microorganisms which contain at most 15 w/w % trehalose, on a dry solid basis (d.s.b.). While the latter enables the separation of trehalose itself with a relative easiness, but it is theoretically difficult to increase the trehalose yield by allowing enzymes to act on substrates at a considerably-high concentration because the enzymatic reaction per se is an equilibrium reaction of 2 different types of enzymes and the equilibrium point constantly inclines to the side of forming glucose phosphate.

In view of the foregoing, the present inventors energetically screened enzymes which form saccharides having a trehalose structure from amylaceous saccharides, and found that microorganisms such as those of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 produce an absolutely novel enzyme which forms non-reducing saccharides having

a trehalose structure as an end unit from reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher. Before or after this finding, it was revealed that such non-reducing saccharides are almost quantitatively hydrolyzed into trehalose and glucose and/or maltooligosaccharides by other enzymes produced from the same microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36. Since the combination use of such enzymes enables to form a desired amount of trehalose with a relative easiness, the aforementioned objects relating to trehalose would be completely overcome. Insufficient producibility of such enzymes by the microorganisms results in a drawback that a relatively-large scale culture of the microorganisms is inevitable to industrially produce trehalose and/or non-reducing saccharides having a trehalose structure as an end unit.

Recombinant DNA technology has made a remarkable progress in recent years. At present, even an enzyme, whose total amino acid sequence has not yet been revealed, can be readily prepared in a desired amount, if a gene encoding the enzyme was once isolated and the base sequence was decoded, by preparing a recombinant DNA containing a DNA which encodes the enzyme, introducing the recombinant DNA into microorganisms or cells of plants or animals, and culturing the resultant transformants. Under these circumstances, urgently required are the finding of genes which encode these enzymes and the elucidation of their base sequences.

## **SUMMARY OF THE INVENTION**

It is an object of the present invention to provide a DNA which encodes an enzyme that releases trehalose from non-reducing saccharides having a trehalose structure as an end unit.

It is a further object of the present invention to provide a replicable recombinant DNA containing the aforesaid DNA.

It is yet another object of the present invention to provide a transformant which is prepared by introducing the recombinant DNA into an appropriate host.

It is a further object of the present invention to prepare the aforesaid enzyme by the application of the recombinant DNA technology.

It is a further object of the present invention to provide a preparation of the enzyme.

It is a further object of the present invention to provide a method for converting non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher.

The first object of the present invention is attained by a DNA which encodes an enzyme that releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher.

The second object of the present invention is attained by a replicable recombinant DNA which contains the aforesaid DNA and a self-replicable vector.

The third object of the present invention is attained by a transformant prepared by introducing the aforesaid self-replicable vector into an appropriate host.

The fourth object of the present invention is attained by a recombinant enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher.

The fifth object of the present invention is attained by a process to produce the recombinant enzyme comprising

culturing a transformant capable of forming the enzyme in a nutrient culture medium, and recovering the formed enzyme from the resultant culture.

The sixth object of the present invention is attained by a method for converting non-reducing saccharides containing a step of allowing the recombinant enzyme to act on non-reducing saccharides, having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, to release trehalose from the saccharides.

#### BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWINGS

FIG. 1 shows the optimum temperature of an enzyme derived from *Rhizobium* sp. M-11.

FIG. 2 shows the optimum temperature of an enzyme derived from *Arthrobacter* sp. Q36.

FIG. 3 shows the optimum pH of an enzyme derived from *Rhizobium* sp. M-11.

FIG. 4 shows the optimum pH of an enzyme derived from *Arthrobacter* sp. Q36.

FIG. 5 shows the thermal stability of an enzyme derived from *Rhizobium* sp. M-11.

FIG. 6 shows the thermal stability of an enzyme derived from *Arthrobacter* sp. Q36.

FIG. 7 shows the pH stability of an enzyme derived from *Rhizobium* sp. M-11.

FIG. 8 shows the pH stability of an enzyme derived from *Arthrobacter* sp. Q36.

FIG. 9 shows the restriction map of the recombinant DNA pBMU27 according to the present invention. In the figure, the bold-lined part is a DNA encoding an enzyme derived from *Rhizobium* sp. M-11.

FIG. 10 shows the restriction map of the recombinant DNA pBRT32 according to the present invention. In the figure, the bold-lined part is a DNA encoding an enzyme derived from *Arthrobacter* sp. Q36.

#### DETAILED DESCRIPTION OF THE INVENTION

The DNA according to the present invention exerts the production of the enzyme encoded by the DNA in a manner that the DNA is inserted into an appropriate self-replicable vector to form a replicable recombinant DNA, followed by introducing the recombinant DNA into a host, incapable of producing the enzyme per se but readily replicable, to form a transformant.

Although the recombinant DNA per se does not produce the enzyme, the production of the enzyme encoded by the DNA is attained by introducing the recombinant DNA into a host, incapable of producing the enzyme but replicable with a relative easiness, to form a transformant, and culturing the transformant to produce the enzyme.

The transformant according to the present invention produces the enzyme when cultured.

The recombinant enzyme according to the present invention releases trehalose when acts on non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher.

The recombinant enzyme is readily obtained in a desired amount by culturing the transformant according to the invention.

Non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization

of 3 or higher are converted into trehalose and glucose and/or maltooligosaccharides.

The present invention is based on the finding of a novel enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher. Such an enzyme can be obtained from cultures of microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36, and the present inventors isolated the enzyme by the combination use of conventional purification methods using column chromatography mainly, examined the properties and features, and revealed the reality, i.e. it is a polypeptide having the following physicochemical properties:

- (1) Action Releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher;
- (2) Molecular weight About 57,000–68,000 daltons on sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE);
- (3) Isoelectric point About 3.3–4.6 on isoelectrophoresis;
- (4) Optimum temperature Exhibiting an optimum temperature of around 35°–45° C. when incubated at pH 7.0 for 30 min;
- (5) Optimum pH Exhibiting an optimum pH of around 6.0–7.5 when incubated at 40° C. for 30 min;
- (6) Thermal stability Stable up to a temperature of around 30°–45° C. when incubated at pH 7.0 for 60 min; and
- (7) pH Stability Stable up to a pH of around 5.5–10.0 when incubated at 25° C. for 16 hours.

Experiments, which were conducted to reveal the physicochemical properties of the enzymes produced by microorganisms of the species *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 (the enzymes from *Rhizobium* sp. M-11 and *Arthrobacter* sp. Q36 are respectively designated as “enzyme M-11” and “enzyme Q36” hereinafter), are explained in the below:

#### Experiment 1

##### Purification of enzyme

##### Experiment 1-1

##### Purification of enzyme M-11

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid culture medium (pH 7.0) containing 2.0 w/v % “PINE-DEX #4”, a starch hydrolysate commercialized by Matsutani Chemical Ind., Co., Ltd., Tokyo, Japan, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate, and 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120° C. for 20 min to effect sterilization. After cooling the flasks a seed culture of *Rhizobium* sp. M-11 was inoculated into each liquid culture medium in each flask, followed by the incubation at 27° C. for 24 hours under rotary-shaking conditions. Twenty L of a fresh preparation of the same liquid culture medium was put in a 30-L jar fermentor and sterilized, followed by inoculating one v/v % of the culture obtained in the above into the sterilized liquid culture medium in the jar fermentor, and incubating it at a pH of 6–8 and 30° C. for 24 hours under aeration-agitation conditions.

Thereafter, about 18 L of the resultant culture was subjected to an ultra-high pressure cell disrupting apparatus to disrupt cells. The resultant suspension was centrifuged to obtain a supernatant, and to about 16 L of which was added ammonium sulfate to give a 20 w/v % saturation, followed by the standing at 4° C. for one hour and the centrifugation to remove sediment. To the resultant supernatant was added ammonium sulfate to give a 60 w/v % saturation, and the

solution was allowed to stand at 4° C. for 24 hours and centrifuged to collect sediment which was then dissolved in a minimum amount of 10 mM phosphate buffer (pH 7.0). The solution thus obtained was dialyzed against 10 mM phosphate buffer (pH 7.0) for 24 hours, and centrifuged to remove insoluble substances. The resultant supernatant was fed to a column packed with "DEAE-TOYOPEARL®", a product for ion-exchange chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 10 mM phosphate buffer (pH 7.0), followed by feeding to the column a linear gradient buffer of sodium chloride ranging from 0 M to 0.5 M in 10 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, dialyzed for 10 hours against 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, and centrifuged to remove insoluble substances. Thereafter, the resultant supernatant was fed to a column, which had been packed with "BUTYL TOYOPEARL®", a gel for hydrophobic column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, and equilibrated with 50 mM phosphate buffer (pH 7.0) containing 2 M ammonium sulfate, followed by feeding to the column a linear gradient buffer of ammonium sulfate ranging from 2 M to 0 mM in 50 mM phosphate buffer (pH 7.0). Fractions containing the objective enzyme were collected from the eluate, pooled, fed to a column packed with "TOYOPEARL® HW-55", a product for gel filtration column chromatography commercialized by Tosoh Corporation, Tokyo, Japan, which had been previously equilibrated with 50 mM phosphate buffer (pH 7.0), followed by feeding to the column 50 mM phosphate buffer (pH 7.0) and collecting fractions containing the objective enzyme. The enzyme thus obtained had a specific activity of about 240 units/mg protein, and the yield was about 650 units per L of the culture.

Throughout the specification the enzyme activity is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltotriosyltrehalose in a test tube, add one ml of an enzyme solution to the tube, and incubate the resultant solution at 40° C. for 30 min to effect enzymatic reaction. Thereafter, one ml of the reaction mixture is mixed with 2 ml of copper reagent to suspend the enzymatic reaction, followed by assaying the reducing activity by the Somogyi-Nelson's method. As a control, an enzyme, which has been previously inactivated by heating at 100° C. for 10 min, is similarly treated as above. One unit activity of the enzyme is defined as the amount of enzyme which increases the reducing power corresponding to one  $\mu$ mol glucose per min under the above conditions.

#### Experiment 1-2

#### Purification of enzyme Q36

Similarly as in Experiment 1-1, a seed culture of *Arthro-bacter* sp. Q36 was cultured, and the resultant culture was treated to obtain a purified enzyme Q36 having a specific activity of about 450 units/mg protein in a yield of about 650 units per L of the culture.

#### Experiment 2

#### Physicochemical property of enzyme

#### Experiment 2-1

#### Action

According to the method disclosed in Japanese Patent Application No.349,216/93, a non-reducing saccharide containing 98 w/w % or higher, d.s.b.,  $\alpha$ -glucosyltrehalose,  $\alpha$ -maltosyltrehalose,  $\alpha$ -maltotriosyltrehalose,  $\alpha$ -maltotetraosyltrehalose or  $\alpha$ -maltopentaosyltrehalose. Either of the non-reducing saccharides as a substrate was

dissolved in 50 mM phosphate buffer (pH 7.0) into a 20 w/v % solution which was then mixed with 2 units/g substrate of the purified enzyme M-11. or Q36 in Experiment 1 and subjected to an enzymatic reaction at 40° C. for 48 hours. The reaction mixture was desalted in usual manner, fed to "WB-T-330", a column for high-performance liquid chromatography (HPLC) commercialized by Wako Pure Chemical Industries, Ltd., Tokyo, Japan, followed by feeding to the column distilled water at a flow rate of 0.5 ml/min at ambient temperature to isolate saccharides contained in the reaction mixture while monitoring the saccharide concentration of the eluate with "MODEL RI-8012", a differential refractometer commercialized by Tosoh Corporation, Tokyo, Japan. As a control, an aqueous solution which contains either maltotriose, maltotetraose, maltopentaose, maltohexaose or maltoheptaose was similarly treated as above, and the resultant mixture was analyzed. The saccharide compositions of the reaction mixtures were tabulated in Tables 1 and 2.

TABLE 1

Substrate	Saccharide in reaction mixture	Saccharide composition (%)
$\alpha$ -Glucosyltrehalose	Trehalose	17.5
	Glucose	6.5
$\alpha$ -Maltosyltrehalose	$\alpha$ -Glucosyltrehalose	76.0
	Trehalose	44.3
	Maltose	44.4
$\alpha$ -Maltotriosyltrehalose	$\alpha$ -Maltosyltrehalose	11.3
	Trehalose	39.5
	Maltotriose	60.0
$\alpha$ -Maltotetraosyltrehalose	$\alpha$ -Maltotriosyltrehalose	0.5
	Trehalose	34.2
	Maltotetraose	65.5
$\alpha$ -Maltopentaosyltrehalose	$\alpha$ -Maltotetraosyltrehalose	0.3
	Trehalose	29.1
	Maltopentaose	70.6
Maltotriose	$\alpha$ -Maltopentaosyltrehalose	0.3
	Maltotriose	100.0
	Maltotetraose	100.0
	Maltopentaose	100.0
	Maltohexaose	100.0
Maltoheptaose	Maltoheptaose	100.0

TABLE 2

Substrate	Saccharide in reaction mixture	Saccharide composition (%)
$\alpha$ -Glucosyltrehalose	Trehalose	19.3
	Glucose	10.2
	$\alpha$ -Glucosyltrehalose	70.5
$\alpha$ -Maltosyltrehalose	Trehalose	44.5
	Maltose	44.4
	$\alpha$ -Maltosyltrehalose	11.1
$\alpha$ -Maltotriosyltrehalose	Trehalose	38.8
	Maltotriose	60.7
	$\alpha$ -Maltotriosyltrehalose	0.5
$\alpha$ -Maltotetraosyltrehalose	Trehalose	34.1
	Maltotetraose	65.7
	$\alpha$ -Maltotetraosyltrehalose	0.2
$\alpha$ -Maltopentaosyltrehalose	Trehalose	29.3
	Maltopentaose	70.4
	$\alpha$ -Maltopentaosyltrehalose	0.3
Maltotriose	Maltotriose	100.0
	Maltotetraose	100.0
	Maltopentaose	100.0
	Maltohexaose	100.0
	Maltoheptaose	100.0

As shown in Tables 1 and 2, enzymes M-11 and Q36 almost quantitatively released trehalose, glucose and maltooligosaccharides from non-reducing saccharides having a

trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher. These enzymes did not act on maltooligosaccharides, as a substrate, having a degree of glucose polymerization of 3 or higher. These facts indicate that these enzymes selectively act on non-reducing saccharides having a trehalose structure as an end unit and specifically hydrolyze the glycosidic bond between trehalose- and glycosyl-residues. Such an enzyme has never been reported and is estimated to have a novel enzymatic reaction mechanism.

#### Experiment 2-2

##### Molecular weight

In accordance with the method reported by U. K. Laemmli in *Nature*, Vol.227, pp.680-685 (1970), the purified enzymes M-11 and Q36 in Experiment 1 were respectively electrophoresed on sodium dodecyl sulfate polyacrylamide gel electrophoresis to show a single protein band at a position corresponding to about 57,000-68,000 daltons. The marker proteins used in this experiment were myosin (MW=200,000 daltons),  $\beta$ -galactosidase (MW=116,250 daltons), phosphorylase B (MW=97,400 daltons), serum albumin (MW=66,200 daltons) and ovalbumin (MW=45,000 daltons).

#### Experiment 2-3

##### Isoelectric point

The purified enzymes M-11 and Q36 obtained in Experiment 1 gave an isoelectric point of about 3.3-4.6 on isoelectrophoresis.

#### Experiment 2-4

##### Optimum temperature

The optimum temperature of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 35°-45° C. as shown in FIGS. 1 and 2 when incubated in usual manner in 50 mM phosphate buffer (pH 7.0) for 30 min.

#### Experiment 2-5

##### Optimum pH

The optimum pH of the purified enzymes M-11 and Q36 obtained in Experiment 1 was about 6.0-7.5 as shown in FIGS. 3 and 4 when experimented in usual manner by incubating them at 40° C. for 30 min in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

#### Experiment 2-6

##### Thermal stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a temperature of about 30°-45° C. as shown in FIGS. 5 and 6 when experimented in usual manner by incubating them in 50 mM phosphate buffer (pH 7.0) for 60 min.

#### Experiment 2-7

##### pH Stability

The purified enzymes M-11 and Q36 obtained in Experiment 1 were stable up to a pH of about 5.5-10.0 as shown in FIGS. 7 and 8 when experimented in usual manner by incubating them at 25° C. for 16 hours in 50 mM acetate buffer, phosphate buffer or sodium carbonate-sodium hydrogen carbonate buffer having different pHs.

#### Experiment 2-8

##### Amino acid sequence containing the N-terminal

The amino acid sequence containing the N-terminal of the purified enzyme M-11 obtained in Experiment 1 was analyzed on "MODEL 470A", a gas-phase protein sequencer commercialized by Applied Biosystems, Inc., Foster City, USA, to reveal that it has the amino acid sequence as shown in SEQ ID NO: 5.

The amino acid sequence containing the N-terminal of the purified enzyme Q36 was analyzed similarly as above to reveal that it has the amino acid sequence as shown in SEQ ID NO: 6.

#### Experiment 2-9

##### Partial amino acid sequence

An adequate amount of the purified enzyme M-11 obtained in Experiment 1-1 was weighed, dialyzed against 10 mM Tris-HCl buffer (pH 9.0) at 4° C. for 18 hours, and admixed with 10 mM Tris-HCl buffer (pH 9.0) to give a concentration of about one mg/ml of the enzyme. About one ml of the resultant solution was placed in a container, admixed with 10  $\mu$ g lysyl endopeptidase, and incubated at 30° C. for 22 hours to partially hydrolyze the enzyme. The resultant hydrolysate was applied to "CAPCELL-PAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Shiseido Co., Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 16 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate at a flow rate of 0.9 ml/min while increasing the concentration of acetonitrile from 16 v/v % to 64 v/v % to separately collect fractions containing a peptide fragment eluted about 43 min or about 57 min after the initiation of feeding (the peptide fragments were respectively named "peptide fragment A" and "peptide fragment B"). Fractions containing the peptide fragment A or B were separately pooled, dried in vacuo, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Similarly as in Experiment 2-8, the peptide fragments A and B were analyzed to reveal that they have the amino acid sequences as shown in SEQ ID NOs: 7 and 8, respectively.

Similarly as in enzyme M-11, enzyme Q36 obtained in Experiment 1-2 was partially hydrolyzed, and the resultant was fed to " $\mu$ BONDAPAK C18", a column for reverse-phase high-performance liquid chromatography commercialized by Japan Millipore Ltd., Tokyo, Japan, which had been previously equilibrated with 0.1 v/v % trifluoroacetate containing 24 v/v % aqueous acetonitrile, followed by feeding to the column 0.1 v/v % trifluoroacetate containing 24 v/v % aqueous acetonitrile while increasing the concentration of aqueous acetonitrile from 24 v/v % to 44 v/v % at a flow rate of 0.9 ml/min. Fractions containing a peptide fragment eluted about 4 min or about 24 min after the initiation of feeding (the fractions were respectively called "peptide fragment C" and "peptide fragment D" hereinafter) were respectively collected, pooled, dried in vacuo, and dissolved in 0.1 v/v % trifluoroacetate containing 50 v/v % aqueous acetonitrile. Analyses of the peptide fragments C and D conducted similarly as above have revealed that they have amino acid sequences as shown in SEQ ID NOs: 9 and 10 respectively.

No enzyme having these physicochemical properties has been known, and this concluded that it is a novel substance. Referring to *Rhizobium* sp. M-11, it is a microorganism which was isolated from a soil of Okayama-city, Okayama, Japan, deposited on Dec. 24, 1992, in National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology, Tsukuba, Ibaraki, Japan, and accepted under the accession number of FERM BP-4130, and it has been maintained by the institute. *Arthrobacter* sp. Q36 is a microorganism which was isolated from a soil of Soja-city, Okayama, Japan, deposited on Jun. 3, 1993, in the same institute, and accepted under the accession number of FERM BP-4316, and it has been maintained by the institute. Japanese Patent Application No.340,343/93, applied by the same applicant, discloses the properties and features of the non-reducing saccharide-forming enzyme as well as the detailed bacteriological properties of these microorganisms.

The present inventors energetically screened the chromosomal DNA of *Rhizobium* sp. M-11 by using an oligonucle-

otide as a probe which had been chemically synthesized based on the partial amino acid sequence of enzyme M-11 as revealed in Experiment 2-8 or 2-9, and obtained a DNA fragment which consists of 1,767 base pairs having the base sequence as shown in the following SEQ ID NO: 1 that initiates from the 5'-terminus. The decoding of the base sequence of the enzyme has revealed that it has an amino acid sequence consisting of 589 amino acids as shown in SEQ ID NO: 2.

Similarly as in enzyme M-11, the chromosomal DNA of enzyme Q36 was screened by using an oligonucleotide as a probe which had been chemically synthesized based on a partial amino acid sequence of enzyme Q36, and this yielded a DNA fragment having a base sequence consisting of 1,791 base pairs as shown in SEQ ID NO: 3. The base sequence was decoded to reveal that enzyme Q36 has an amino acid sequence consisting of 597 amino acids as shown in SEQ ID NO: 4.

The sequential experimental steps used for revealing the base sequence and amino acid sequence as shown in SEQ ID NOs: 1 to 4 are summarized as below:

- (1) The enzyme was isolated from a culture of a donor microorganism and highly purified. The purified enzyme was partially hydrolyzed with protease, and the resultant 2 different types of peptide fragments were isolated and determined their amino acid sequences;
- (2) Separately, a chromosomal DNA was isolated from a donor microorganism's cell, purified and partially digested by a restriction enzyme to obtain a DNA fragment consisting of about 2,000–6,000 base pairs. The DNA fragment was ligated by DNA ligase to a plasmid vector, which had been previously cut with a restriction enzyme, to obtain a recombinant DNA;
- (3) The recombinant DNA was introduced into *Escherichia coli* to obtain transformants, and from which an objective transformant containing a DNA encoding the enzyme was selected by the colony hybridization method using an oligonucleotide, as a probe, which had been chemically synthesized based on the aforesaid partial amino acid sequence; and
- (4) The recombinant DNA was obtained from the selected transformant and annealed with a primer, followed by allowing a DNA polymerase to act on the resultant to extend the primer, and determining the base sequence of the resultant complementary chain DNA by the dideoxy chain termination method. The comparison of an amino acid sequence, estimable from the determined base sequence with the aforesaid amino acid sequence, confirmed that the base sequence encodes the enzyme.

The recombinant enzyme as referred to in the specification mean the whole recombinant enzymes which are preparable by the recombinant DNA technology and capable of releasing trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher. Generally, the recombinant enzyme according to the present invention has a revealed amino acid sequence, and, as an example, the amino acid sequence as shown in SEQ ID NO: 2 or 4 which initiates from the N-terminal, as well as homologous ones to it, can be mentioned. Variants having amino acid sequences homologous to the one as shown in SEQ ID NO: 2 or 4 can be obtained by replacing one or more amino acids in SEQ ID NO: 2 or 4 with other amino acids without substantially altering the inherent activity of the enzyme. Although even when used the same DNA and it also depends on hosts into which the DNA is introduced, as well as on ingredients and components of nutrient culture media used for culturing

transformants, and their cultivation temperature and pH, there may be produced modified enzymes which have amino acid sequences similar to that of SEQ ID NO: 2 or 4, as well as having the enzymatic activity inherent to the enzyme encoded by the DNA but defective one or more amino acids located near to the N-terminal of the amino acid sequence of SEQ ID NO: 2 or 4 and/or having one or more amino acids newly added to the N-terminal by the modification of intracellular enzymes of host s after the DNA expression. In view of the technical background in the art, the enzyme as referred to in the present invention includes those which have the amino acid sequence corresponding to that of SEQ ID NO: 2 or 4, and those which substantially have the amino acid sequence as shown in SEQ ID NO: 2 or 4 except that one or more amino acids in the amino acid sequence are defected, newly added to or replaced with other amino acids, as long as they release trehalose form non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher.

In this field, it is known that one or more bases in DNAs can be replaced with other bases by the degeneracy of genetic code without altering the amino acid sequences encoded by the DNAs. Based on this the DNA according to the present invention includes DNAs which contain the base sequence of SEQ ID NO: 1 or 3 and other DNAs, wherein one or more bases are replaced with other bases by degeneracy of genetic code, as long as they encode enzymes having the amino acid sequence as shown in SEQ ID NO: 2 or 4 and homologous variants thereof.

According to the today's recombinant DNA technology, the determination of base sequences from the 5'-termini of DNAs define their complementary base sequences. Therefore, the DNA according to the present invention also includes complementary base sequences corresponding to any one of the aforesaid base sequences. Needless to say, one or more bases in the base sequence, which encodes the enzyme or their variants, can be readily replaced with other bases to allow the DNA to actually express the enzyme production in hosts.

The DNA according to the present invention is as described above, and any DNA derived from natural resources and those artificially synthesized can be used in the present invention as long as they have the aforementioned base sequences. The natural resources of the DNA according to the present invention are, for example, microorganisms of the genera *Rhizobium*, *Arthrobacter*, *Brevibacterium* and *Micrococcus*, i.e. *Rhizobium* sp. M-11 (FERM BP-4130), *Arthrobacter* sp. Q36 (FERM BP-4316), *Brevibacterium helvolum* (ATCC 11822) and *Micrococcus roseus* (ATCC 186) from which genes containing the present DNA can be obtained. These microorganisms can be inoculated in nutrient culture media and cultured for about 1–3 days under aerobic conditions, and the resultant cells were collected from the cultures and subjected to ultrasonication or treated with a cell-wall lysis enzyme such as lysozyme or  $\beta$ -glucanase to extract genes containing the present DNA. In this case, a proteolytic enzyme such as protease can be used along with the cell-wall lysis enzyme, and, in the case of treating the cells with ultrasonication, they may be treated in the presence of a surfactant such as sodium dodecyl sulfate (SDS) or treated with freezing- and thawing-methods. The objective DNA is obtainable by treating the resultant with phenol extraction, alcohol sedimentation, centrifugation, protease treatment and/or ribonuclease treatment used in general in the art.

To artificially synthesize the DNA according to the present invention, it can be chemically synthesized by using

the base sequence as shown in SEQ ID NO: 1 or 3, or can be obtained in plasmid form by inserting a DNA, which encodes the amino acid sequence as shown in SEQ ID NO: 2 or 4, into an appropriate self-replicable vector to obtain a recombinant DNA, introducing the recombinant DNA into an appropriate host to obtain a transformant, culturing the transformant, separating the proliferated cells from the resultant culture, and collecting plasmids containing the DNA from the cells.

The present invention further relates to replicable recombinant DNAs which express the production of the enzyme according to the invention when introduced into microorganisms as well as plant- and animal-cells which do not produce the enzyme inherently but are readily proliferative. Such a recombinant DNA, which generally contains the aforesaid DNA and a self-replicable vector, can be prepared by conventional method with a relative easiness when the material DNA is in hand. Examples of such a vector are plasmid vectors such as pBR322, pUC18, Bluescript II SK(+), pUB110, pTZ4, pCI94, pHV14, TRp7, TEp7, pBS7, etc.; and phage vectors such as  $\lambda$ gt- $\lambda$ C,  $\lambda$ gt- $\lambda$ B,  $\rho$ 11,  $\phi$ 1,  $\phi$ 105, etc. Among these plasmid- and phage-vectors, pBR322, pUC18, Bluescript II SK(+),  $\lambda$ gt- $\lambda$ C and  $\lambda$ gt- $\lambda$ B are satisfactorily used in case that the present DNA should be expressed in *Escherichia coli*, while pUB110, pTZ4, pCI94,  $\rho$ 11,  $\phi$ 1 and  $\phi$ 105 are satisfactorily used to express the DNA in microorganisms of the genus *Bacillus*. The plasmid vectors pHV14, TRp7, TEp7 and pBS7 are suitably used when the recombinant DNA is allowed to grow in 2 or more hosts.

The methods used to insert the present DNA into such vectors in the present invention may be conventional ones generally used in this field. A gene containing the present DNA and a self-replicable vector are first digested by a restriction enzyme and/or ultrasonic disintegrator, then the resultant DNA fragments and vector fragments are ligated. To digest DNAs and vectors, restriction enzymes which specifically act on nucleotides, particularly, type II restriction enzymes, more particularly, Sau 3AI, Eco RI, Hind III, Bam HI, Sal I, Xba I, Sac I, Pst I, etc., facilitate the ligation of the DNA fragments and vector fragments. The ligation of the DNA fragments and vector fragments is effected by annealing them first if necessary, then subjected to the action of a DNA ligase in vivo or in vitro. The recombinant DNA thus obtained is replicable without substantial limitation by introducing it into appropriate hosts, and culturing the resultant transformants.

The recombinant DNA according to the present invention can be introduced into appropriate host microorganisms including *Escherichia coli* and those of the genus *Bacillus* as well as actinomyces and yeasts. In the case of using *Escherichia coli* as a host, it can be cultured in the presence of the recombinant DNA and calcium ion, while in the case of using the microorganisms of the genus *Bacillus* the competent cell method and the colony hybridization method can be employed. Desired transformants can be cloned by the colony hybridization method or by culturing a variety of transformants in nutrient culture media containing non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, and selecting the objective transformants which release trehalose from the non-reducing saccharides.

The transformants thus obtained extracellularly produce the objective enzyme when cultured in nutrient culture media. Generally, liquid media in general supplemented with carbon sources, nitrogen sources and minerals, and, if necessary, further supplemented with a small amount of

amino acids and vitamins can be used as the nutrient culture media. Examples of the carbon sources are saccharides such as starch, starch hydrolysate, glucose, fructose and sucrose. Examples of the nitrogen sources are organic- and inorganic-substances containing nitrogen such as ammonia, ammonium salts, urea, nitrate, peptone, yeast extract, defatted soy bean, corn steep liquor and beef extract. Cultures containing the objective enzyme can be prepared by inoculating the transformants into nutrient culture media, and incubating them at a temperature of 25°–65° C. and a pH of 2–8 for about 1–6 days under aerobic aeration-agitation conditions. Such a culture can be used intact as an enzyme preparation, and, usually, it may be disrupted with ultrasonic disintegrator and/or cell-wall lysis enzymes prior to use, followed by separating the enzyme from the intact cells and cell debris by filtration and/or centrifugation, and purifying the enzyme. The methods used for purifying the enzyme in the invention include conventional ones in general. From cultures the intact cells and cell debris are eliminated and subjected to one or more methods such as concentration, salting out, dialysis, separately sedimentation, gel filtration chromatography, ion exchange chromatography, hydrophobic chromatography, affinity chromatography, gel electrophoresis and isoelectric point electrophoresis.

As is described above, the enzyme exerts a distinct activity of forming trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher, and such an activity has not yet been found in any conventional enzymes. Therefore, the use of the enzyme facilitates the preparation of trehalose in a relatively-high yield and efficiency from non-reducing saccharides such as  $\alpha$ -glucosyltrehalose,  $\alpha$ -maltosyltrehalose,  $\alpha$ -maltotriosyltrehalose,  $\alpha$ -maltotetraosyltrehalose and  $\alpha$ -maltopentaosyltrehalose in a considerably-high yield. These non-reducing saccharides can be obtained in a satisfactorily-high yield from starch hydrolysates, which are obtained by treating amylaceous substances such as starch, amylose and amylopectin prepared with acids and/or amylases, by using non-reducing saccharide-forming enzyme as disclosed in Japanese Patent Application No.349,216/93. Thus, trehalose, whose industrial preparation has been difficult, can be prepared from starch and amylaceous substances as a material with a relative easiness and in a desired amount when the present enzyme and the non-reducing saccharide-forming enzyme, as disclosed in Japanese Patent Application No.349,216/93, are used in combination.

As described in "Handbook of Amylases and Related Enzymes", 1st edition, edited by The Amylase Research Society of Japan, published by Pergamon Press plc, Oxford, England (1988),  $\alpha$ -amylase, maltotetraose-forming amylase, maltopentaose-forming amylase and maltohexaose-forming amylase are especially useful to prepare the reducing amylaceous saccharides used in the invention, and, the use of any one of these amylases readily yields amylaceous saccharide mixtures rich in reducing amylaceous saccharides having a degree of glucose polymerization of 3 or higher in a considerably-high yield. If necessary, the combination use of such an amylase and a starch debranching enzyme such as pullulanase or isoamylase can increase the yield of the reducing amylaceous saccharides usable as a substrate for the non-reducing saccharide-forming enzyme, i.e. the non-reducing saccharides can be obtained by coexisting the non-reducing saccharide-forming enzyme in an aqueous solution containing as a substrate one or more of the reducing amylaceous saccharides in an amount up to a concentration of 50 w/v %, 65



and subjecting the solution to an enzymatic reaction at a temperature of about 40°–55° C. and a pH of about 6–8 until a desired amount of the objective non-reducing saccharides are formed.

Usually, in the present conversion method, the recombinant enzyme according to the present invention is allowed to coexist in the aforesaid aqueous solution containing one or more of the non-reducing amylaceous saccharides, and to enzymatically react with the saccharides while keeping at a prescribed temperature and pH until a desired amount of trehalose is released.

Although the enzymatic reaction proceeds even below a concentration of 0.1 w/v % of a substrate, a higher concentration of 2 w/v %, preferably, 5–50 w/v % of a substrate can be satisfactorily used to apply the present conversion method to an industrial-scale production. The temperature and pH used in the enzymatic reaction are set within the ranges of which do not inactivate the recombinant enzyme and allow the recombinant enzyme to effectively act on substrates, i.e. a temperature up to about 55° C., preferably, a temperature in the range of about 40°–55° C., and a pH of 5–10, preferably, a pH in the range of about 6–8. The amount and reaction time of the present recombinant enzyme are chosen dependently on the enzymatic reaction conditions. The enzymatic reaction effectively converts non-reducing saccharides into saccharide compositions containing trehalose and glucose and/or maltooligosaccharides, and, in the case of using  $\alpha$ -maltotriosyltrehalose as a substrate, the conversion rate reaches to approximately 100%. In the case of simultaneously subjecting starch hydrolysates to the action of either of the above amylases together with the non-reducing saccharide-forming enzyme and the present recombinant enzyme, non-reducing saccharides are formed from the hydrolysates while hydrolyzed into glucose and/or maltooligosaccharides, and because of this saccharide compositions with a relatively-high trehalose content can be effectively obtained in a relatively-high yield.

The reaction products obtained by the present conversion reaction can be used intact, and, usually, they are purified prior to use: Insoluble substances are eliminated from the reaction products by filtration and centrifugation, and the resultant solutions are decolored with activated charcoal, desalted and purified on ion exchangers, and concentrated into syrupy products. Dependently on their use, the syrupy products are dried in vacuo and spray-dried into solid products. In order to obtain products which substantially consist of non-reducing saccharides, the above mentioned syrupy products are subjected to one or more methods such as chromatography using an ion exchanger, activated charcoal and silica gel to separate saccharides, separately sedimentation using alcohol and/or acetone, membrane filtration, fermentation by yeasts, and removal and decomposition of reducing saccharides by alkalis. The methods to treat a large amount of reaction mixture are, for example, fixed bed- or pseudomoving bed-ion exchange column chromatography as disclosed in Japanese Patent Laid-Open Nos. 23,799/83 and 72,598/83, and such a method enables an effective industrial-scale production of products with a relatively-high trehalose content.

These trehalose and compositions containing the same have a wide applicability to a variety of products which are apt to be readily damaged by the reducibility of saccharide sweeteners: For example, they can be satisfactorily used as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant in food products in general, cosmetics and pharmaceuticals.

The following examples explain the present invention in more detail, and the techniques themselves used in the

examples are conventional ones in this field, for example, those described by J. Sumbruck et al. in “*Molecular Cloning A Laboratory Manual*”, 2nd edition, published by Cold Spring Harbor Laboratory Press (1989).

#### Example 1

Preparation of recombinant DNA containing DNA encoding enzyme M-11 and transformant

##### Example 1-1

Preparation of chromosomal DNA

A seed culture of *Rhizobium* sp. M-11 was inoculated into bacto nutrient broth medium (pH 7.0), and cultured at 27° C. for 24 hours with a rotary shaker. The cells were separated from the resultant culture by centrifugation, suspended in TES buffer (pH 8.0), admixed with 0.05 w/v % lysozyme, and incubated at 37° C. for 30 min. The resultant was freezed at –80° C. for one hour, admixed with TSS buffer (pH 9.0), heated to 60° C., and further admixed with a mixture solution of TES buffer and phenol, and the resultant solution was chilled with ice, followed by centrifugally collecting the precipitated crude chromosomal DNA. To the supernatant was added 2 fold volumes of cold ethanol, and the re-precipitated crude chromosomal DNA was collected, suspended in SSC buffer (pH 7.1), admixed with 7.5  $\mu$ g ribonuclease and 125  $\mu$ g protease, and incubated at 37° C. for one hour. Thereafter, a mixture solution of chloroform and isoamyl alcohol was added to the reaction mixture to extract the objective chromosomal DNA, and admixed with cold ethanol, followed by collecting the formed sediment containing the chromosomal DNA. The purified chromosomal DNA thus obtained was dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was freezed at –80° C.

##### Example 1-2

Preparation of recombinant DNA pBMU27 and transformant BMU27

About one ml of the purified chromosomal DNA obtained in Example 1-1 was placed in a container, admixed with about 35 units of Sau 3AI, a restriction enzyme, and enzymatically reacted at 37° C. for about 20 min to partially digest the chromosomal DNA, followed by recovering a DNA fragment consisting of about 2,000–6,000 base pairs by means of sucrose density-gradient ultracentrifugation. One  $\mu$ g of Bluescript II SK(+), a plasmid vector, was provided, subjected to the action of Bam HI, a restriction enzyme, to completely digest the plasmid vector, admixed with 10  $\mu$ g of the DNA fragment and 2 units of T4 DNA ligase, and allowed to stand at 4° C. overnight to ligate the DNA fragment to the vector fragment. To the resultant recombinant DNA was added 30  $\mu$ l of “Epicurian Coli@ XLI-Blue”, competent cell commercialized by Toyobo Co., Ltd., Tokyo, Japan, allowed to stand under ice-chilling conditions for 30 min, heated to 42° C., admixed with SOC broth, and incubated at 37° C. for one hour to introduce the recombinant DNA into *Escherichia coli*.

The resultant transformant was inoculated into agar plate (pH 7.0) containing 50  $\mu$ g/ml of 5-bromo-4-chloro-3-indolyl- $\beta$ -galactoside, and cultured at 37° C. for 18 hours, followed by placing a nylon film on the agar plate to fix thereon about 6,000 colonies formed on the agar plate. Based on the amino acid sequence located at positions from 8 to 13 as shown in SEQ ID No: 7, i.e. Phe-Asp-Ile-Trp-Ala-Pro, the base sequence of probe 1 represented by 5'-TTYGAYATHTGGGCNCC-3' (SEQ ID NO: 15) was chemically synthesized, labelled with <sup>32</sup>P, and hybridized with the colonies of transformants fixed on the nylon film, followed by selecting 14 transformants which exhibited a strong hybridization.

The objective recombinant DNA was selected in usual manner from the 14 transformants, and, in accordance with the method described by E. M. Southern in *Journal of Molecular Biology*, Vol.98, pp.503-517 (1975), the recombinant DNA was hybridized with probe 2 having the base sequence as shown in SEQ ID NO: 8, which had been chemically synthesized based on the amino acid sequence located at positions from 2 to 6, i.e. Asp-Trp-Ala-Glu-Ala, in SEQ ID NO: 8, followed by selecting a recombinant DNA strongly hybridized with the probe 2. The recombinant DNA and transformant thus selected were respectively named "pBMU27" and "BMU27".

The transformant BMU27 was inoculated into L-broth (pH 7.0) containing 100 µg/ml ampicillin, and cultured at 37° C. for 24 hours by a rotary shaker. After completion of the culture, the resultant cells were collected from the culture by centrifugation, and treated with the alkaline method in general to extracellularly extract a recombinant DNA. The extract was in usual manner purified and analyzed to reveal that the recombinant DNA pBMU27 consists of about 5,700 base pairs and has the structure expressed by the restriction map as shown in FIG. 9. It was found that, as shown in FIG. 9, the DNA which consists of 1,767 base pairs for encoding the enzyme M-11 is positioned in the downstream near to the digested site of Eco RV, a restriction enzyme.

#### Example 1-3

##### Production of enzyme by transformant BMU27

A liquid nutrient culture medium consisting of 2.0 w/v % "PINE-DEX #4", a starch hydrolysate commercialized by Matsutani Chemical Ind., Co., Ltd., Tokyo, Japan, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50 µg/ml ampicillin, autoclaved at 120° C. for 20 min, cooled and inoculated with a seed culture of transformant BMU27 obtained in Example 1-2, followed by culturing the transformant at 37° C. for 24 hours by a rotary shaker. The resultant culture was treated with ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to find that one L of the culture yielded about 4,000 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Rhizobium* sp. M-11 was inoculated in the same fresh preparation of the same liquid nutrient culture medium but free of ampicillin, and, in the case of culturing *Rhizobium* sp. M-11, it was cultured and treated similarly as above except that the cultivation temperature was set to 30° C. Assaying the resultant activity, one L culture of *Rhizobium* sp. M-11 yielded about 2,000 units of the enzyme, and the yield was significantly lower than that of transformant BMU27. *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BMU27 was purified similarly as in Experiment 1-1, and examined on the properties and characters. As a result, it was revealed that it has substantially the same physicochemical properties as enzyme M-11, i.e. it has a molecular weight of about 57,000-68,000 daltons on SDS-PAGE and an isoelectric point of about 3.3-4.6 on isoelectrophoresis. The results indicate that the present enzyme can be prepared by the recombinant DNA technology, and the yield can be significantly increased thereby.

#### Example 2

Preparation of complementary chain DNA derived from *Rhizobium* sp. M-11, and determination for its base sequence and amino acid sequence

Two µg of the recombinant DNA pBMU27 obtained in Example 1-2 was provided, admixed with 2 M aqueous sodium hydroxide solution to effect degeneration, and admixed with an adequate amount of cold ethanol, followed by collecting the formed sediment containing a template DNA and drying the sediment in vacuo. To the template DNA were added 50 pmole/ml of a chemically synthesized primer 1 represented by 5'-GTAAAACGACGGCCAGT-3' (SEQ ID NO: 16), 10 µl of 40 mM Tris-HCl buffer (pH 7.5) containing 20 mM magnesium chloride and 20 mM sodium chloride, and the mixture was incubated at 65° C. for 2 min to effect annealing and admixed with 2 µl of an aqueous solution containing dATP, dGTP and dTTP in respective amounts of 7.5 µM, 0.5 µl of [ $\alpha$ -<sup>32</sup>P]dCTP (2 mCi/ml), one µl of 0.1 M dithiothreitol, and 2 µl of 1.5 units/ml T7 DNA polymerase, followed by incubating the resultant mixture at 25° C. for 5 min to extend the primer 1 from the 5'-terminus to the 3'-terminus. Thus, a complementary chain DNA was formed.

The reaction product containing the complementary chain DNA was divided into quarters, to each of which 2.5 µl of 50 mM aqueous sodium chloride solution containing 80 µM dNTP and 8 µM ddATP, ddCTP, ddGTP or ddTTP was added, and the resultant mixture was incubated at 37° C. for 5 min, followed by suspending the reaction by the addition of 4 µl of 98 v/v % aqueous formamide solution containing 20 mM EDTA, 0.05 w/v % bromophenol blue, and 0.05 w/v % xylene cyanol. The reaction mixture was heated with a boiling-water bath for 3 min, and a portion of which was placed on a gel containing 6 w/v % polyacrylamide, and electrophoresed by energizing the gel with a constant voltage of about 2,000 volts to separate DNA fragments, followed by fixing the gel in usual manner, drying the gel and subjecting the resultant gel to autoradiography.

Analyses of the DNA fragments separated on the radio-gram revealed that the complementary chain DNA contains the base sequence consisting of about 2,161 base pairs as shown in SEQ ID NO: 11. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO: 12 and was compared with the amino acid sequence containing the N-terminal or the partial amino acid sequence of enzyme M-11 as shown in SEQ ID NO: 5, 7 or 8. As a result, it was found that the amino acid sequence containing the N-terminal of SEQ ID NO: 5 corresponds to the amino acid sequence located at positions from 8 to 27 in SEQ ID NO: 12, and the partial amino acid sequence of SEQ ID NO: 7 or 8 corresponds to the amino acid sequence located at positions from 10 to 30 or at positions from 493 to 509 in SEQ ID NO: 12. These results indicate that enzyme M-11 has the amino acid sequence of SEQ ID NO: 2, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO: 1.

#### Example 3

Preparation of recombinant DNA, containing DNA derived from *Arthrobacter* sp. Q36, and transformant

##### Example 3-1

##### Preparation of chromosomal DNA

Similarly as in Example 1-1, a chromosomal DNA was isolated from *Arthrobacter* sp. Q36, purified and dissolved in SSC buffer (pH 7.1) to give a concentration of about one mg/ml, and the resultant solution was freeze-dried at -80° C. for storage.

##### Example 3-2

Preparation of recombinant DNA pBRT32 and transformant BRT32

The purified chromosomal DNA obtained in Example 3-1 was partially digested similarly as in Example 1-2, followed

by recovering a DNA fragment consisting of about 2,000–6,000 base pairs by sucrose density gradient ultracentrifugation. The DNA fragment was ligated to a lysate of Bluescript II SK(+) which had been treated with Bam HI, and the resultant recombinant DNA was introduced into *Escherichia coli* XLI-Blue. The transformants thus obtained were cultured similarly as in Example 1-2 on agar plates containing 5-bromo-4-chloro-3-indolyl- $\beta$ -galactoside, and the formed about 5,000 colonies were fixed on a nylon film, while the probe 3 represented by 5'-ATGGGNTGGGAYCCNGC-3' (SEQ ID NO: 17) was chemically synthesized based on the amino acid sequence of Met-Gly-Trp-Asp-Pro-Ala located at positions from 5 to 10 in SEQ ID NO: 9, labelled with  $^{32}$ P, and hybridized with transformant colonies which had been fixed on the nylon film, followed by selecting 10 transformants which strongly hybridized with the probe 3.

Similarly as in Example 1-2, the objective recombinant DNA was selected from 10 transformants, and hybridized with probe 4 represented by 5'-TAYGAYGTNTGGGC-3' (SEQ ID NO: 18) which had been chemically synthesized based on the amino acid sequence of Tyr-Asp-Val-Trp-Ala located at positions from 8 to 12 in SEQ ID NO: 10, followed by selecting a recombinant DNA which strongly hybridized with probe 4. The recombinant DNA and transformant thus selected were respectively named "pBRT32" and "BRT32".

The transformant BRT32 was inoculated into L-broth containing ampicillin, and cultured similarly as in Example 1-2, and the proliferated cells were collected from the resultant culture, and from which a recombinant DNA was extracted, purified and analyzed to reveal that the recombinant DNA pBRT32 consists of about 6,200 base pairs and has the structure of the restriction map as shown in FIG. 10. As shown in FIG. 10, it was revealed that the DNA, which consists of 1,791 base pairs for encoding the DNA of enzyme Q36, is located in the downstream near to the cleavage site of Kpn I.

#### Example 3-3

##### Production of enzyme by transformant BRT32

A liquid nutrient culture medium consisting of 2.0 w/v % "PINE-DEX #4", a starch hydrolysate commercialized by Matsutani Chemical Ind., Co., Ltd., Tokyo, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate was adjusted to pH 7.0, admixed with 50  $\mu$ g/ml ampicillin, autoclaved at 120° C. for 20 min, cooled and inoculated with a seed culture of the transformant BRT32 obtained in Example 3-2, followed by culturing the transformant at 37° C. for 24 hours by a rotary shaker. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the present enzyme activity to find that one L of the culture yielded about 3,900 units of the enzyme.

As a control, a seed culture of *Escherichia coli* XLI-Blue or *Arthrobacter* sp. Q36 was inoculated into a fresh preparation of the same liquid nutrient culture medium but free of ampicillin, and, in the case of culturing *Arthrobacter* sp. Q36, it was cultured and treated similarly as above except that the cultivation temperature was set to 30° C. Assaying the enzyme activity, one L of the culture of *Arthrobacter* sp. Q36 yielded about 1,800 units of the enzyme, and the yield was significantly lower than that of the transformant BRT32. The *Escherichia coli* XLI-Blue used as a host did not form the enzyme.

Thereafter, the enzyme produced by the transformant BRT32 was purified similarly as in Experiment 1-1, and

examined on the properties and characters to reveal that it has substantially the same physicochemical properties as that of enzyme Q36, i.e. it has a molecular weight of about 57,000–68,000 daltons on SDS-PAGE and an isoelectric point of about 3.3–4.6 on isoelectrophoresis. These results indicate that the enzyme can be prepared by the recombinant DNA technology, and the yield can be significantly increased thereby.

#### Example 4

Preparation of complementary chain DNA derived from *Arthrobacter* sp. Q36, and determination for its base sequence and amino acid sequence

The recombinant DNA pBRT32 obtained in Example 3-2 was similarly treated as in Example 2 to form a template DNA which was then annealed together with the primer 1, followed by allowing T7 DNA polymerase to act on the resultant to extend the primer 1 from the 5'-terminus to the 3'-terminus to obtain a complementary chain DNA. Similarly as in Example 2, the complementary chain DNA was subjected to the dideoxy chain terminator method to analyze DNA fragments which had been isolated on a radiogram. The result revealed that the complementary chain DNA contained a base sequence consisting of 2,056 base pairs as shown in SEQ ID NO: 13. An amino acid sequence estimable from the base sequence was as shown in SEQ ID NO: 14, and compared with the amino acid sequence containing the N-terminal or the partial amino acid sequence of SEQ ID NO: 6, 9 or 10. As a result, it was found that the amino acid sequence of SEQ ID NO: 6 corresponds to that located at positions from 2 to 21 in SEQ ID NO: 14, and that the partial amino acid sequence in SEQ ID NO: 9 or 10 corresponds to that located at positions from 470 to 489 or at positions from 12–31 in SEQ ID NO: 14. These results indicate that enzyme Q36 has the amino acid sequence of SEQ ID NO: 4, and it is encoded by the DNA having the base sequence as shown in SEQ ID NO: 3.

#### Example 5

##### Preparation of recombinant enzyme

In 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid nutrient culture medium (pH 7.0) consisting of 2.0 w/v % "PINE-DEX#4", a starch hydrolysate commercialized by Matsutani Chemical Ind., Co., Ltd., Tokyo, Japan, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and to each flask was added 50  $\mu$ g/ml ampicillin and autoclaved at 120° C. for 20 min. Thereafter, the flasks were cooled and inoculated with a seed culture of the transformant BMU27 obtained in Example 1-2, followed by culturing the transformant at 27° C. for 24 hours by a rotary shaker. Apart from this, 18 L of a fresh preparation of the same liquid culture medium was placed in a 30-L jar fermentor, admixed with 50  $\mu$ g/ml ampicillin, sterilized at 120° C. for 20 min, cooled and inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 37° C. for 24 hours while keeping the pH at 6–8 under aeration-agitation conditions. The resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances. The supernatant thus obtained was assayed for the enzyme activity to reveal that one L of the culture yielded about 3,900 units of the enzyme. The supernatant was purified by the method in Experiment 1-1 to obtain an about 67 ml aqueous solution containing an about 165 units/ml of a recombinant enzyme having a specific activity of about 290 units/mg protein.

## Example 6

## Preparation of recombinant enzyme

Recombinant BRT32 obtained by the method in Experiment 3-2 was cultured similarly as in Example 5, and the resultant culture was treated with an ultrasonic integrator to disrupt cells. The resultant suspension was centrifuged to remove insoluble substances, and the resultant supernatant was assayed for the enzyme activity to have an activity of about 4,000 units per L. The supernatant was purified by the method in Experiment 1-1 to obtain an about 55 ml aqueous solution containing about 200 units/ml of a recombinant enzyme with a specific activity of about 420 units/mg protein.

## Example 7

## Conversion of non-reducing saccharide by recombinant enzyme

## Example 7-1 (a)

## Preparation of non-reducing saccharide-forming enzyme

To 500-ml Erlenmeyer flasks were placed 100 ml aliquots of a liquid nutrient culture medium (pH 7.0) consisting of 2.0 w/v % maltose, 0.5 w/v % peptone, 0.1 w/v % yeast extract, 0.1 w/v % disodium hydrogen phosphate and 0.1 w/v % potassium dihydrogen phosphate, and the flasks were autoclaved at 120° C. for 20 min. Thereafter, the flasks were cooled and inoculated with a seed culture of *Rhizobium* sp. M-11, followed by culturing it at 27° C. for 24 hours by a rotary shaker. Apart from this, 20 L of a fresh preparation of the same liquid culture medium was placed in a 30-L jar fermentor, and sterilized, inoculated with one v/v % of the seed culture obtained in the above, followed by the culture at 30° C. and at a pH of 7-8 for 24 hours under aeration-agitation conditions. Thereafter, the resultant culture was treated with an ultrasonic disintegrator to disrupt cells, and the resultant suspension was centrifuged to remove insoluble substances and purified according to the method in Experiment 1-1 to obtain a non-reducing saccharide-forming enzyme having a specific activity of about 195 units/mg protein in a yield of about 220 units per L of the culture.

Throughout the specification the activity of a non-reducing saccharide-forming enzyme is expressed by the value measured on the following assay: Place 4 ml of 50 mM phosphate buffer (pH 7.0) containing 1.25 w/v % maltopentaose in a test tube, add one ml of an enzyme solution to the test tube, and incubate the solution at 40° C. for 60 min to effect enzymatic reaction. Thereafter, the reaction mixture is heated at 100° C. for 10 min to suspend the enzymatic reaction, followed by diluting it with distilled water by 10 times and assaying the reducing activity by the Somogyi-Nelson's method. One unit activity of the non-reducing saccharide-forming enzyme is defined as the amount of enzyme which decreases the reducing power corresponding to one  $\mu$ mol maltopentaose per min under the above conditions.

## Example 7-1(b)

## Preparation of syrupy product containing trehalose

A potato starch was suspended in water to give a 15 w/w % suspension which was then mixed with 0.1 w/w % calcium carbonate. The mixture was adjusted its pH to 6.0, mixed with 0.2 w/w %, d.s.b., of "TERMAMYL 60L", an  $\alpha$ -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted at 95° C. for 15 min to effect gelatinization and

liquefaction. The liquefied solution was autoclaved at 120° C. for 30 min to inactivate the remaining enzyme, rapidly cooled to 45° C., 1,000 units/g starch, d.s.b., of pullulanase commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, 3.4 units/g starch, d.s.b., of the non-reducing saccharide-forming enzyme obtained in Example 7-1(a), and 4.2 units/g starch, d.s.b., of the recombinant enzyme obtained by the method in Example 5, followed the enzymatic reaction for 48 hours. The reaction mixture was heated at 95° C. for 10 min to inactivate the remaining enzyme, cooled, filtered, and, in usual manner, decolorized with an activated charcoal, desalted and purified with an ion-exchange resin, and concentrated to obtain a syrupy product with a concentration of about 60 w/w % in a yield of about 92%, d.s.b.

Analysis of the syrup by the method of Experiment 2-1 revealed that it contained 70.2 w/w % trehalose, 2.4 w/w %  $\alpha$ -glucosyltrehalose, 3.3 w/w %  $\alpha$ -maltosyltrehalose, 0.7 w/w % glucose, 10.1 w/w % maltose, 12.9 w/w % maltotriose, and 0.4 w/w % maltooligosaccharides having a degree of glucose polymerization of 4 or higher. The product, having a mild and moderate sweetness as well as an adequate viscosity and moisture-retaining ability, can be satisfactorily used in food products in general, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## Example 7-1(c)

## Preparation of powdery product containing trehalose

To 4 jacketed-stainless steel columns, having a diameter of 5.4 cm and a length of 5 m each was packed homogeneity with "XT-1016 (Na<sup>+</sup>-form)", a strong-acid cation exchange resin commercialized by Tokyo Organic Chemical Industries, Ltd., Tokyo, Japan, and the columns were cascaded in series to give a total column length of 20 m. The syrupy product obtained in Example 7-1(b) was fed to the columns at a rate of about 5 v/v % against the resin at an inner column temperature of 55° C., and the columns were fed with 55° C. hot water at an SV (space velocity) 0.3 to fractionate saccharides in the syrupy product. Based on the analysis of the saccharide composition of the eluate, fractions rich in trehalose were collected, pooled, concentrated, dried in vacuo and pulverized to obtain a solid product containing about 97 w/w % trehalose in a yield of about 56% against the starting material, d.s.b.

The product, having a mild sweetness and substantially free of reducibility, can be satisfactorily used in food products in general, cosmetics and pharmaceuticals as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

## Example 7-1(d)

## Preparation of powdery crystalline trehalose

A portion of the trehalose rich fraction obtained in Example 7-1(c) was concentrated into an about 75 w/w % solution which was then transferred to a crystallizer, admixed with about 2 w/w %, d.s.b., hydrous crystalline trehalose as a seed crystal, and crystallized under gentle stirring conditions to obtain a masseccuite with a crystallinity of about 45 w/w %. The masseccuite was sprayed downward from a nozzle, equipped at the upper part of a spraying tower at a pressure of about 150 kg/cm<sup>2</sup> while about 85° C. hot air was flowing downward from the upper part of the tower to

accumulate a crystalline powder on a belt conveyer provided on the basement of the tower, followed by gradually transferring it out of the tower. Thereafter, the powder was transferred to an ageing tower and aged for 10 hours to complete the crystallization and drying while an about 40° C. hot air was blowing to the contents. Thus, a powdery product containing hydrous crystalline trehalose was obtained in a yield of about 90 w/w % against the starting material, d.s.b.

The product, having a substantial non-hygroscopicity and a mild and high-quality sweetness, can be satisfactorily used in food products in general, cosmetics, pharmaceuticals and feeds as a sweetener, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

#### Example 8

Conversion of non-reducing saccharide by recombinant enzyme

Potato starch was suspended in water to give a concentration of 6 w/w %, d.s.b., and the suspension was admixed with 500 units/g starch of isoamylase commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, and enzymatically reacted for 20 hours. The reaction mixture was adjusted to a pH of 6.5, autoclaved at 120° C. for 10 min to inactivate the remaining enzyme, rapidly cooled to 95° C., admixed with 0.1 w/w % per g starch, d.s.b., of "TERMAMYL 60L", an  $\alpha$ -amylase specimen commercialized by Novo Nordisk Bioindustri A/S, Copenhagen, Denmark, and enzymatically reacted for 15 min. The reaction mixture was heated at 130° C. for 30 min to inactivate the remaining enzyme, rapidly cooled to 45° C., admixed with 4.1 units/g starch, d.s.b., of a non-reducing saccharide-forming enzyme obtained by the method in Example 7-1(a), and 4.9 units/g starch, d.s.b., of the present recombinant enzyme obtained by the method in Example 6, and enzymatically reacted for 64 hours. The reaction mixture was heated at 95° C. for 10 min to inactivate the remaining enzyme, rapidly cooled to 55° C., adjusted to pH 5.0, admixed with 10 units/g starch, d.s.b., of "GLUCOZYME", a glucoamylase specimen commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 95° C. for 10 min to inactivate the remaining enzyme, cooled, filtered, and, in usual manner, decolorized with an activated charcoal, desalted and purified with an ion-exchange resin, and concentrated to obtain an about 60 w/w % syrupy product containing about 80.5 w/w % trehalose, d.s.b. The syrupy product was concentrated into an about 84 w/w % syrup which was then transferred to a crystallizer, admixed with an about 2 w/w % hydrous crystalline trehalose, d.s.b., and crystallized under gentle stirring conditions to obtain a masseccuite having a crystallinity of about 45 w/w %. The masseccuite was distributed to plastic plain vessels which were then allowed to stand at ambient temperature for 3 days to effect solidification and aging, followed by detaching the resultant blocks from the vessels and pulverizing the blocks with a cutter to obtain a solid product containing hydrous crystalline trehalose in a yield of about 90 w/w % against the material starch, d.s.b.

The product, which is substantially free of hygroscopicity and readily handleable, can be arbitrarily used in food products in general, cosmetics, pharmaceuticals as a sweet-

ening agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

#### Example 9

Conversion of non-reducing saccharide by recombinant enzyme

Potato starch was suspended in water to give a concentration of 6 w/w %, d.s.b., and the suspension was admixed with 0.01 w/w % "NEO-SPITASE",  $\alpha$ -amylase commercialized by Nagase Biochemicals, Ltd., Kyoto, Japan, adjusted to pH 6.2, and enzymatically reacted at 85°-90° C. for 20 min to gelatinize and liquefy the starch. The liquefied starch was heated at 120° C. for 10 min to inactivate the remaining enzyme, rapidly cooled to 45° C., admixed with 500 units/g starch, d.s.b., of isoamylase commercialized by Hayashibara Biochemical Laboratories, Inc., Okayama, Japan, 3.2 units/g starch, d.s.b., of a non-reducing saccharide-forming enzyme obtained by the method in Example 7-1(a), and 5.0 units/g starch, d.s.b., of the present recombinant enzyme obtained by the method in Example 5, and enzymatically reacted for 48 hours. The reaction mixture was heated at 95° C. for 10 min to inactivate the remaining enzyme, rapidly cooled to 55° C., adjusted to pH 5.0, admixed with 10 units/g starch, d.s.b., of "GLUCOZYME", glucoamylase commercialized by Nagase Biochemicals Ltd., Kyoto, Japan, and enzymatically reacted for 40 hours. The reaction mixture was heated at 95° C. for 10 min to inactivate the remaining enzyme, rapidly cooled, filtered, and, in usual manner, decolorized with an activated charcoal, desalted and purified with an ion-exchange resin, and concentrated to give a concentration of about 60 w/w %, d.s.b., to obtain a syrupy product containing 78.3 w/w % trehalose, d.s.b. The syrupy product was fractionated similarly as in Example 7-1(c) except for using "CG6000(Na<sup>+</sup>)", a strong-acid cation exchange resin commercialized by Japan Organo, Co., Ltd., Tokyo, Japan, to obtain a fraction containing about 95 w/w % trehalose, d.s.b. The fraction was concentrated to give a concentration of about 75 w/w %, d.s.b., and, similarly as in Example 8, crystallized, and the resultant masseccuite in the form of block was pulverized to obtain a powdery product containing hydrous crystalline trehalose in a yield of about 70 w/w % against the material starch, d.s.b.

The product, which is substantially free of hygroscopicity and readily handleable, can be arbitrarily used in food products in general, cosmetics, pharmaceuticals as a sweetening agent, taste-improving agent, quality-improving agent, stabilizer, filler, excipient and adjuvant.

As is described above, the present invention is based on the finding that a novel enzyme which releases trehalose from non-reducing saccharides having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher. The present invention is to explore a way to produce the enzyme in a relatively-large scale and in a considerably-high yield. The enzyme produced by the transformant according to the present invention is the one characterized by its revealed total amino acid sequence, and because of this it can be used for the preparations of trehalose which is premised on being used in food products without fear of causing side effects.

Therefore, the present invention is an useful invention which exerts the aforesaid significant action and effect as well as giving a great contribution to this field.

## SEQUENCE LISTING

## ( 1 ) GENERAL INFORMATION:

( i i i ) NUMBER OF SEQUENCES: 18

## ( 2 ) INFORMATION FOR SEQ ID NO:1:

## ( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 1767 base pairs

( B ) TYPE: nucleic acid

( C ) STRANDEDNESS: single

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

## ( i x ) FEATURE:

( A ) NAME/KEY: CDS

( B ) LOCATION: 1..1767

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GCA	GGC	ACC	GTA	ACG	CTG	CTG	GCC	GGC	GGG	GAG	CGC	TAC	GAG	ATG	GGC	9 6
Ala	Gly	Thr	Val	Thr	Leu	Leu	Ala	Gly	Gly	Glu	Arg	Tyr	Glu	Met	Gly	
			20					25					30			
CGC	CGC	CCC	GGC	AAC	GGG	CCG	GCG	GAC	GAA	GGC	TGG	TGG	ACG	GCC	GCG	14 4
Arg	Arg	Pro	Gly	Asn	Gly	Pro	Ala	Asp	Glu	Gly	Trp	Trp	Thr	Ala	Ala	
		35					40				45					
GAT	GCA	CCG	ACA	GGC	GCG	GAC	GTG	GAC	TAC	GGA	TAC	CTG	CTC	GAC	GGC	19 2
Asp	Ala	Pro	Thr	Gly	Ala	Asp	Val	Asp	Tyr	Gly	Tyr	Leu	Leu	Asp	Gly	
	50					55			60							
GAC	GAA	ATC	CCG	CTG	CCG	GAC	CCC	CGG	ACC	CGC	CGC	CAG	CCC	GAA	GGC	24 0
Asp	Glu	Ile	Pro	Leu	Pro	Asp	Pro	Arg	Thr	Arg	Arg	Gln	Pro	Glu	Gly	
65				70				75						80		
GTC	CAT	GCC	CTG	TCC	CGG	ACC	TTC	GAC	CCC	GGC	GCC	CAC	CGC	TGG	CAG	28 8
Val	His	Ala	Leu	Ser	Arg	Thr	Phe	Asp	Pro	Gly	Ala	His	Arg	Trp	Gln	
			85					90					95			
GAC	GCC	GGG	TGG	CAG	GGC	AGG	GAA	CTC	CAG	GGC	TCC	GTG	ATT	TAC	GAA	33 6
Asp	Ala	Gly	Trp	Gln	Gly	Arg	Glu	Gln	Gly	Ser	Val	Ile	Tyr	Glu		
		100					105					110				
CTC	CAC	ATC	GGA	ACG	TTC	ACG	CCG	GAA	GGG	ACG	CTG	GAC	GCC	GCC	GCG	38 4
Leu	His	Ile	Gly	Thr	Phe	Thr	Pro	Glu	Gly	Thr	Leu	Asp	Ala	Ala	Ala	
	115						120				125					
GGC	AAG	CTG	GAC	TAC	CTC	GCC	GGC	CTG	GGC	ATC	GAC	TTC	ATT	GAG	CTG	43 2
Gly	Lys	Leu	Asp	Tyr	Leu	Ala	Gly	Leu	Gly	Ile	Asp	Phe	Ile	Glu	Leu	
	130					135				140						
CTG	CCC	GTG	AAT	GCC	TTC	AAC	GGC	ACG	CAC	AAC	TGG	GGC	TAC	GAC	GGC	48 0
Leu	Pro	Val	Asn	Ala	Phe	Asn	Gly	Thr	His	Asn	Trp	Gly	Tyr	Asp	Gly	
145				150					155					160		
GTC	CAG	TGG	TTT	GCC	GTG	CAT	GAA	GGC	TAC	GGC	GGG	CCT	GCG	GCG	TAC	52 8
Val	Gln	Trp	Phe	Ala	Val	His	Glu	Gly	Tyr	Gly	Gly	Pro	Ala	Ala	Tyr	
			165					170					175			
CAG	CGG	TTC	GTG	GAT	GCG	GCC	CAC	GCG	GCC	GGC	CTC	GGC	GTC	ATC	CAG	57 6
Gln	Arg	Phe	Val	Asp	Ala	Ala	His	Ala	Ala	Gly	Leu	Gly	Val	Ile	Gln	
		180					185						190			
GAC	GTG	GTC	TAC	AAC	CAC	CTC	GGG	CCG	AGC	GGG	AAC	TAC	CTC	CCC	AGG	62 4
Asp	Val	Val	Tyr	Asn	His	Leu	Gly	Pro	Ser	Gly	Asn	Tyr	Leu	Pro	Arg	
	195					200						205				
TAC	GGC	CCG	TAC	CTC	AAG	CAC	GGC	GAA	GGC	AAC	ACC	TGG	GGC	GAT	TCG	67 2
Tyr	Gly	Pro	Tyr	Leu	Lys	His	Gly	Glu	Gly	Asn	Thr	Trp	Gly	Asp	Ser	
	210					215					220					

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GTC Val 225	AAC Asn	CTG Leu	GAC Asp	GGG Gly	CCG Pro 230	GGA Gly	TCC Ser	GAC Asp	CAC His	GTC Val 235	CGC Arg	CAG Gln	TAC Tyr	ATC Ile	CTG Leu 240	720
GAC Asp	AAC Asn	GTG Val	GCC Ala	ATG Met 245	TGG Trp	CTG Leu	CGC Arg	GAC Asp	TAC Tyr 250	CGG Arg	GTG Val	GAC Asp	GGC Gly	CTC Leu 255	CGC Arg	768
CTG Leu	GAC Asp	GCC Ala	GTC Val 260	CAC His	GCC Ala	CTG Leu	AAG Lys	GAT Asp 265	GAG Glu	CGG Arg	GCC Ala	GTC Val	CAC His 270	ATC Ile	CTG Leu	816
GAG Glu	GAG Glu	TTC Phe 275	GGC Gly	GCG Ala	CTG Leu	GCG Ala	GAC Asp 280	GCC Ala	CTG Leu	TCG Ser	TCC Ser	GAA Glu 285	GGC Gly	GGC Gly	CGC Arg	864
CCG Pro	CTG Leu 290	ACC Thr	CTC Leu	ATC Ile	GCC Ala	GAG Glu 295	TCC Ser	GAC Asp	CTC Leu	AAC Asn	AAT Asn 300	CCG Pro	CGG Arg	CTG Leu	CTG Leu	912
TAC Tyr 305	CCC Pro	CGG Arg	GAT Asp	GTC Val	AAC Asn 310	GGC Gly	TAC Tyr	GGA Gly	CTG Leu	GCC Ala 315	GGC Gly	CAG Gln	TGG Trp	AGC Ser	GAC Asp 320	960
GAC Asp	TTC Phe	CAC His	CAC His	GCC Ala 325	GTG Val	CAC His	GTC Val	AAC Asn	GTC Val 330	AGC Ser	GGG Gly	GAA Glu	ACC Thr	ACC Thr 335	GGC Gly	1008
TAC Tyr	TAC Tyr	AGC Ser	GAC Asp 340	TTC Phe	GAC Asp	TCG Ser	CTC Leu	GGA Gly 345	GCC Ala	CTC Leu	GCC Ala	AAG Lys	GTC Val 350	CTG Leu	CGT Arg	1056
GAC Asp	GGG Gly	TTC Phe 355	TTC Phe	CAC His	GAC Asp	GGC Gly	AGC Ser 360	TAC Tyr	TCC Ser	AGC Ser	TTC Phe	CGC Arg 365	GGC Gly	CGC Arg	TGC Cys	1104
CAC His 370	GGC Gly	CGG Arg	CCG Pro	ATC Ile	AAC Asn	TTC Phe 375	AGC Ser	GCC Ala	GTG Val	CAT His	CCG Pro 380	GCC Ala	GCG Ala	CTG Leu	GTG Val	1152
GTC Val 385	TGC Cys	TCA Ser	CAG Gln	AAC Asn	CAT His 390	GAC Asp	CAG Gln	ATC Ile	GGC Gly	AAC Asn 395	CGG Arg	GCC Ala	ACC Thr	GGG Gly	GAC Asp 400	1200
CGG Arg	CTG Leu	TCC Ser	CAG Gln	TCA Ser 405	CTT Leu	CCG Pro	TAC Tyr	GGC Gly	AGC Ser 410	CTG Leu	GCC Ala	CTG Leu	GCC Ala	GCC Ala 415	GTG Val	1248
CTG Leu	ACC Thr	CTC Leu	ACC Thr 420	GGT Gly	CCG Pro	TTC Phe	ACG Thr	CCC Pro 425	ATG Met	CTG Leu	TTC Phe	ATG Met	GGA Gly 430	GAG Glu	GAA Glu	1296
TAC Tyr	GGG Gly	GCC Ala 435	ACC Thr	ACC Thr	CCG Pro	TGG Trp	CAG Gln 440	TTC Phe	TTC Phe	ACC Thr	TCG Ser	CAC His 445	CCT Pro	GAA Glu	CCC Pro	1344
GAG Glu	CTG Leu 450	GGC Gly	AAG Lys	GCC Ala	ACG Thr	GCC Ala 455	GAG Glu	GGC Gly	AGG Arg	ATC Ile	AGG Arg 460	GAG Glu	TTC Phe	GAG Glu	CGC Arg	1392
ATG Met 465	GGG Gly	TGG Trp	GAT Asp	CCC Pro	GCC Ala 470	GTC Val	GTG Val	CCC Pro	GAT Asp	CCG Pro 475	CAG Gln	GAT Asp	CCG Pro	GAG Glu	ACC Thr 480	1440
TTC Phe	ACC Thr	CGC Arg	TCC Ser	AAA Lys 485	CTG Leu	GAC Asp	TGG Trp	GCG Ala	GAA Glu 490	GCG Ala	TCC Ser	GCC Ala	GGC Gly	GAT Asp 495	CAT His	1488
GCC Ala	CGC Arg	CTC Leu	CTG Leu 500	GAG Glu	CTG Leu	TAC Tyr	CGC Arg	TCG Ser 505	CTT Leu	ATC Ile	ACG Thr	CTG Leu	CGG Arg 510	CGG Arg	TCA Ser	1536
ACT Thr	CCG Pro	GAG Glu 515	CTC Leu	GCG Ala	CGC Arg	CTG Leu	GGC Gly 520	TTT Phe	GCG Ala	GAC Asp	ACC Thr	GCC Ala 525	GTC Val	GAG Glu	TTC Phe	1584
GAC Asp	GAC Asp 530	GAC Asp	GCC Ala	CGC Arg	TGG Trp	CTC Leu 535	CGT Arg	TAT Tyr	TGG Trp	CGC Arg	GGA Gly 540	GGC Gly	GTG Val	CAG Gln	GTG Val	1632

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GTG	CTG	AAC	TTC	GCG	GAC	CGT	CCC	ATC	AGC	CTG	GAC	CGG	CCG	GGA	ACC	1 6 8 0
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5 4 5					5 5 0					5 5 5					5 6 0	
GCG	CTG	CTG	CTC	GCC	ACC	GAC	GAC	GCC	GTC	CGG	ATG	GAC	GGA	GTC	CAG	1 7 2 8
Ala	Leu	Leu	Leu	Ala	Thr	Asp	Asp	Ala	Val	Arg	Met	Asp	Gly	Val	Gln	
				5 6 5					5 7 0					5 7 5		
GTG	GAG	CTG	CCG	CCG	CTG	AGC	GCC	GCG	GTT	CTG	CGC	GAC				1 7 6 7
Val	Glu	Leu	Pro	Pro	Leu	Ser	Ala	Ala	Val	Leu	Arg	Asp				
			5 8 0					5 8 5								

( 2 ) INFORMATION FOR SEQ ID NO:2:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 589 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ala	Gly	Thr	Val	Thr	Leu	Leu	Ala	Gly	Gly	Glu	Arg	Tyr	Glu	Met	Gly	
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Arg	Arg	Pro	Gly	Asn	Gly	Pro	Ala	Asp	Glu	Gly	Trp	Trp	Thr	Ala	Ala	
		35					40					45				
Asp	Ala	Pro	Thr	Gly	Ala	Asp	Val	Asp	Tyr	Gly	Tyr	Leu	Leu	Asp	Gly	
	50					55					60					
Asp	Glu	Ile	Pro	Leu	Pro	Asp	Pro	Arg	Thr	Arg	Arg	Gln	Pro	Glu	Gly	
65				70						75					80	
Val	His	Ala	Leu	Ser	Arg	Thr	Phe	Asp	Pro	Gly	Ala	His	Arg	Trp	Gln	
				85					90					95		
Asp	Ala	Gly	Trp	Gln	Gly	Arg	Glu	Leu	Gln	Gly	Ser	Val	Ile	Tyr	Glu	
		100					105						110			
Leu	His	Ile	Gly	Thr	Phe	Thr	Pro	Glu	Gly	Thr	Leu	Asp	Ala	Ala	Ala	
		115					120					125				
Gly	Lys	Leu	Asp	Tyr	Leu	Ala	Gly	Leu	Gly	Ile	Asp	Phe	Ile	Glu	Leu	
	130					135					140					
Leu	Pro	Val	Asn	Ala	Phe	Asn	Gly	Thr	His	Asn	Trp	Gly	Tyr	Asp	Gly	
145					150					155					160	
Val	Gln	Trp	Phe	Ala	Val	His	Glu	Gly	Tyr	Gly	Gly	Pro	Ala	Ala	Tyr	
			165						170					175		
Gln	Arg	Phe	Val	Asp	Ala	Ala	His	Ala	Ala	Gly	Leu	Gly	Val	Ile	Gln	
			180					185					190			
Asp	Val	Val	Tyr	Asn	His	Leu	Gly	Pro	Ser	Gly	Asn	Tyr	Leu	Pro	Arg	
		195					200					205				
Tyr	Gly	Pro	Tyr	Leu	Lys	His	Gly	Glu	Gly	Asn	Thr	Trp	Gly	Asp	Ser	
	210					215					220					
Val	Asn	Leu	Asp	Gly	Pro	Gly	Ser	Asp	His	Val	Arg	Gln	Tyr	Ile	Leu	
225					230					235					240	
Asp	Asn	Val	Ala	Met	Trp	Leu	Arg	Asp	Tyr	Arg	Val	Asp	Gly	Leu	Arg	
			245						250					255		
Leu	Asp	Ala	Val	His	Ala	Leu	Lys	Asp	Glu	Arg	Ala	Val	His	Ile	Leu	
			260					265					270			
Glu	Glu	Phe	Gly	Ala	Leu	Ala	Asp	Ala	Leu	Ser	Ser	Glu	Gly	Gly	Arg	
		275					280					285				
Pro	Leu	Thr	Leu	Ile	Ala	Glu	Ser	Asp	Leu	Asn	Asn	Pro	Arg	Leu	Leu	
	290					295					300					



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Tyr 305	Pro	Arg	Asp	Val	Asn 310	Gly	Tyr	Gly	Leu	Ala 315	Gly	Gln	Trp	Ser	Asp 320
Asp	Phe	His	His	Ala 325	Val	His	Val	Asn 330	Val	Ser	Gly	Glu	Thr	Thr 335	Gly
Tyr	Tyr	Ser	Asp 340	Phe	Asp	Ser	Leu	Gly 345	Ala	Leu	Ala	Lys	Val 350	Leu	Arg
Asp	Gly	Phe 355	Phe	His	Asp	Gly	Ser 360	Tyr	Ser	Ser	Phe	Arg 365	Gly	Arg	Cys
His	Gly 370	Arg	Pro	Ile	Asn 375	Phe	Ser	Ala	Val	His	Pro 380	Ala	Ala	Leu	Val
Val 385	Cys	Ser	Gln	Asn 390	His	Asp	Gln	Ile	Gly	Asn 395	Arg	Ala	Thr	Gly	Asp 400
Arg	Leu	Ser	Gln 405	Ser	Leu	Pro	Tyr	Gly	Ser 410	Leu	Ala	Leu	Ala	Ala 415	Val
Leu	Thr	Leu	Thr 420	Gly	Pro	Phe	Thr	Pro 425	Met	Leu	Phe	Met	Gly 430	Glu	Glu
Tyr	Gly	Ala 435	Thr	Thr	Pro	Trp	Gln 440	Phe	Phe	Thr	Ser	His 445	Pro	Glu	Pro
Glu	Leu 450	Gly	Lys	Ala	Thr	Ala 455	Glu	Gly	Arg	Ile	Arg 460	Glu	Phe	Glu	Arg
Met 465	Gly	Trp	Asp	Pro	Ala 470	Val	Val	Pro	Asp	Pro 475	Gln	Asp	Pro	Glu	Thr 480
Phe	Thr	Arg	Ser	Lys 485	Leu	Asp	Trp	Ala	Glu 490	Ala	Ser	Ala	Gly	Asp 495	His
Ala	Arg	Leu	Leu 500	Glu	Leu	Tyr	Arg	Ser 505	Leu	Ile	Thr	Leu	Arg 510	Arg	Ser
Thr	Pro	Glu 515	Leu	Ala	Arg	Leu	Gly 520	Phe	Ala	Asp	Thr	Ala 525	Val	Glu	Phe
Asp	Asp 530	Asp	Ala	Arg	Trp	Leu 535	Arg	Tyr	Trp	Arg	Gly 540	Gly	Val	Gln	Val
Val 545	Leu	Asn	Phe	Ala	Asp 550	Arg	Pro	Ile	Ser	Leu 555	Asp	Arg	Pro	Gly	Thr 560
Ala	Leu	Leu	Leu	Ala 565	Thr	Asp	Asp	Ala	Val 570	Arg	Met	Asp	Gly	Val 575	Gln
Val	Glu	Leu	Pro 580	Pro	Leu	Ser	Ala	Ala 585	Val	Leu	Arg	Asp			

( 2 ) INFORMATION FOR SEQ ID NO:3:

( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 1791 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: single  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( i x ) FEATURE:  
 ( A ) NAME/KEY: CDS  
 ( B ) LOCATION: 1..1791

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACG Thr 590	CAC His	ACC Thr	TAC Tyr	CCG Pro	CGG Arg 595	GAA Glu	GCC Ala	GCG Ala	AAA Lys	CCC Pro 600	GTC Val	CTG Leu	GGC Gly	CCC Pro	GCA Ala 605	48
CGC Arg	TAC Tyr	GAC Asp	GTC Val	TGG Trp 610	GCG Ala	CCC Pro	AAC Asn	GCT Ala	GAA Glu 615	TCC Ser	GTG Val	ACG Thr	CTG Leu	CTG Leu	GCC Ala 620	96

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GGC Gly	GGG Gly	GAG Glu	CGC Arg 625	TAC Tyr	GCC Ala	ATG Met	CAG Gln	CGC Arg 630	CGG Arg	GCC Ala	GAG Glu	ACC Thr	GGG Gly 635	CCG Pro	GAG Glu	144
GAC Asp	GCC Ala	GGC Gly 640	TGG Trp	TGG Trp	ACC Thr	GCC Ala	GCC Ala 645	GGC Gly	GCG Ala	CCT Pro	ACG Thr	GAT Asp 650	GGC Gly	AAC Asn	GTG Val	192
GAC Asp	TAC Tyr 655	GGG Gly	TAC Tyr	CTT Leu	CTG Leu	GAC Asp 660	GGC Gly	GAC Asp	GAA Glu	ACA Thr	CCG Pro 665	CTT Leu	CCG Pro	GAT Asp	CCA Pro	240
CGG Arg 670	ACC Thr	CGC Arg	CGC Arg	CAG Gln	CCC Pro 675	GAC Asp	GGC Gly	GTC Val	CAC His	GCC Ala 680	CTG Leu	TCC Ser	CGC Arg	ACG Thr	TTC Phe 685	288
GAC Asp	CCG Pro	TCC Ser	GCG Ala	TAC Tyr 690	AGC Ser	TGG Trp	CAG Gln	GAC Asp 695	GAC Asp	GCC Ala	TGG Trp	CAG Gln	GGC Gly	AGG Arg 700	GAA Glu	336
CTG Leu	CAG Gln	GGC Gly	GCC Ala 705	GTC Val	ATC Ile	TAC Tyr	GAG Glu	CTC Leu 710	CAC His	CTC Leu	GGA Gly	ACA Thr	TTC Phe 715	ACG Thr	CCC Pro	384
GAA Glu	GGG Gly	ACG Thr 720	CTG Leu	GAG Glu	GCG Ala	GCC Ala	GCC Ala 725	GGA Gly	AAG Lys	CTG Leu	GAC Asp 730	TAC Tyr 730	CTC Leu	GCC Ala	GGC Gly	432
TTG Leu	GGC Gly 735	GTC Val	GAC Asp	TTC Phe	ATC Ile	GAG Glu 740	CTG Leu	CTG Leu	CCG Pro	GTG Val	AAC Asn 745	GCT Ala	TTC Phe	AAC Asn	GGC Gly	480
ACG Thr 750	CAC His	AAC Asn	TGG Trp	GGT Gly	TAC Tyr 755	GAC Asp	GGT Gly	GTC Val	CAG Gln	TGG Trp 760	TTC Phe	GCT Ala	GTG Val	CAC His	GAG Glu 765	528
GCA Ala	TAC Tyr	GGC Gly	GGG Gly	CCG Pro 770	GAA Glu	GCG Ala	TAC Tyr	CAG Gln	CGG Arg 775	TTC Phe	GTC Val	GAC Asp	GCC Ala 780	GCC Ala	CAC His	576
GCC Ala	GCA Ala	GGC Gly	CTT Leu 785	GGC Gly	GTG Val	ATC Ile	CAG Gln	GAC Asp 790	GTG Val	GTC Val	TAC Tyr	AAC Asn	CAC His 795	CTC Leu	GGC Gly	624
CCC Pro	AGC Ser	GGG Gly 800	AAC Asn	TAC Tyr	CTG Leu	CCG Pro	CGG Arg 805	TTC Phe	GGG Gly	CCG Pro	TAC Tyr	CTC Leu 810	AAG Lys	CAG Gln	GGC Gly	672
GAG Glu	GGT Gly 815	AAC Asn	ACG Thr	TGG Trp	GGC Gly	GAC Asp 820	TCG Ser	GTG Val	AAC Asn	CTG Leu	GAC Asp 825	GGG Gly	CCC Pro	GGC Gly	TCC Ser	720
GAC Asp 830	CAT His	GTG Val	CGC Arg	CGG Arg	TAC Tyr 835	ATC Ile	CTG Leu	GAC Asp	AAC Asn	CTG Leu 840	GCC Ala	ATG Met	TGG Trp	CTG Leu	CGT Arg 845	768
GAC Asp	TAC Tyr	CGG Arg	GTG Val	GAC Asp 850	GGC Gly	CTG Leu	CGG Arg	CTG Leu	GAC Asp 855	GCC Ala	GTC Val	CAC His	GCC Ala	CTG Leu 860	AAG Lys	816
GAT Asp	GAG Glu	CGG Arg	GCG Ala 865	GTG Val	CAC His	ATC Ile	CTG Leu	GAG Glu 870	GAC Asp	TTC Phe	GGG Gly	GCG Ala	CTG Leu 875	GCC Ala	GAT Asp	864
CAG Gln	ATC Ile	TCC Ser 880	GCC Ala	GAG Glu	GTG Val	GGA Gly	CGG Arg 885	CCG Pro	CTG Leu	ACG Thr	CTC Leu	ATC Ile 890	GCC Ala	GAG Glu	TCC Ser	912
GAC Asp	CTC Leu 895	AAC Asn	AAC Asn	CCG Pro	CGG Arg	CTG Leu 900	CTG Leu	TAC Tyr	CCG Pro	CGG Arg	GAC Asp 905	GTC Val	AAC Asn	GGG Gly	TAC Tyr	960
GGG Gly 910	CTG Leu	GAA Glu	GGG Gly	CAG Gln	TGG Trp 915	AGC Ser	GAC Asp	GAC Asp	TTC Phe	CAC His 920	CAC His	GCC Ala	GTC Val	CAC His	GTC Val 925	1008
AAC Asn	GTC Val	ACC Thr	GGC Gly	GAA Glu 930	ACC Thr	ACC Thr	GGC Gly	TAC Tyr 935	TAC Tyr 935	AGT Ser	GAC Asp	TTC Phe	GAC Asp	TCG Ser 940	CTG Leu	1056

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GCC Ala	GCC Ala	CTC Leu	GCC Ala 945	AAG Lys	GTG Val	CTC Leu	CGG Arg	GAC Asp 950	GGC Gly	TTC Phe	TTC Phe	CAC His	GAC Asp 955	GGC Gly	AGC Ser	1104
TAC Tyr	TCC Ser	AGC Ser 960	TTC Phe	CGG Arg	GAA Glu	CGC Arg	CAC His 965	CAC His	GGA Gly	CGG Arg	CCG Pro	ATT Ile 970	AAT Asn	TTC Phe	AGC Ser	1152
GCC Ala	GTA Val 975	CAC His	CCA Pro	GCC Ala	GCC Ala	CTG Leu 980	GTG Val	GTC Val	TGT Cys	TCG Ser	CAG Gln 985	AAC Asn	CAC His	GAC Asp	CAG Gln	1200
ATC Ile 990	GGC Gly	AAC Asn	CGT Arg	GCC Ala	ACG Thr 995	GGG Gly	GAC Asp	CGG Arg	CTC Leu	TCC Ser 1000	CAG Gln	ACC Thr	CTG Leu	CCG Pro	TAC Tyr 1005	1248
GGA Gly	AGC Ser	CTG Leu	GCC Ala	CTC Leu 1010	GCT Ala	GCG Ala	GTG Val	CTG Leu	ACC Thr 1015	CTG Leu	ACG Thr	GGA Gly	CCC Pro	TTC Phe 1020	ACG Thr	1296
CCC Pro	ATG Met	CTG Leu	CTC Leu 1025	ATG Met	GGC Gly	GAG Glu	GAG Glu	TAC Tyr 1030	GGC Gly	GCC Ala	AGC Ser	ACG Thr	CCG Pro 1035	TGG Trp	CAG Gln	1344
TTT Phe	TTC Phe	ACC Thr 1040	TCG Ser	CAC His	CCG Pro	GAG Glu	CCG Pro 1045	GAG Glu	CTC Leu	GGC Gly	AAG Lys	GCC Ala 1050	ACC Thr	GCG Ala	GAG Glu	1392
GGC Gly	CGG Arg 1055	ATC Ile	AAG Lys	GAG Glu	TTC Phe	GAG Glu 1060	CGC Arg	ATG Met	GGG Gly	TGG Trp	GAT Asp 1065	CCC Pro	GCC Ala	GTC Val	GTG Val	1440
CCC Pro 1070	GAT Asp	CCC Pro	CAG Gln	GAT Asp	CCT Pro 1075	GAG Glu	ACG Thr	TTC Phe	CGC Arg	CGG Arg 1080	TCC Ser	AAG Lys	CTG Leu	GAC Asp	TGG Trp 1085	1488
GCG Ala	GAA Glu	GCC Ala	GCC Ala	GAA Glu 1090	GGC Gly	GAC Asp	CAT His	GCC Ala	CGG Arg 1095	CTG Leu	CTG Leu	GAG Glu	CTG Leu	TAC Tyr 1100	CGT Arg	1536
TCG Ser	CTC Leu	ACC Thr 1105	GCC Ala	CTG Leu	CGC Arg	CGC Arg	TCC Ser	ACG Thr 1110	CCG Pro	GAC Asp	CTC Leu	ACC Thr	AAG Lys 1115	CTG Leu	GGC Gly	1584
TTC Phe	GAG Glu	GAC Asp 1120	ACG Thr	CAG Gln	GTG Val	GCG Ala	TTC Phe 1125	GAC Asp	GAG Glu	GAC Asp	GCC Ala	CGC Arg 1130	TGG Trp	CTG Leu	CGG Arg	1632
TTC Phe	CGC Arg 1135	CGG Arg	GGT Gly	GGC Gly	GTG Val	CAG Gln 1140	GTG Val	CTG Leu	CTC Leu	AAC Asn	TTC Phe 1145	TCG Ser	GAA Glu	CAG Gln	CCC Pro	1680
GTG Val 1150	AGC Ser	CTG Leu	GAC Asp	GGG Gly	GCG Ala 1155	GGC Gly	ACG Thr	GCC Ala	CTG Leu	CTG Leu 1160	CTG Leu	GCC Ala	ACC Thr	GAC Asp	GAC Asp 1165	1728
GCC Ala	GTC Val	CGG Arg	CTA Leu	GAA Glu 1170	GGT Gly	GAG Glu	CGT Arg	GCG Ala	GAA Glu 1175	CTC Leu	GGT Gly	CCG Pro	CTG Leu	AGC Ser 1180	GCC Ala	1776
GCC Ala	GTC Val	GTC Val	AGC Ser 1185	GAC Asp												1791

( 2 ) INFORMATION FOR SEQ ID NO:4:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 597 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr His Thr Tyr Pro Arg Glu Ala Ala Lys Pro Val Leu Gly Pro Ala  
1 5 10 15

Arg Tyr Asp Val Trp Ala Pro Asn Ala Glu Ser Val Thr Leu Leu Ala

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20							25					30			
Gly	Gly	Glu 35	Arg	Tyr	Ala	Met	Gln 40	Arg	Arg	Ala	Glu	Thr 45	Gly	Pro	Glu
Asp	Ala 50	Gly	Trp	Trp	Thr	Ala 55	Ala	Gly	Ala	Pro	Thr 60	Asp	Gly	Asn	Val
Asp 65	Tyr	Gly	Tyr	Leu	Leu 70	Asp	Gly	Asp	Glu	Thr 75	Pro	Leu	Pro	Asp	Pro 80
Arg	Thr	Arg	Arg	Gln 85	Pro	Asp	Gly	Val	His 90	Ala	Leu	Ser	Arg	Thr 95	Phe
Asp	Pro	Ser	Ala 100	Tyr	Ser	Trp	Gln	Asp 105	Asp	Ala	Trp	Gln	Gly 110	Arg	Glu
Leu	Gln	Gly 115	Ala	Val	Ile	Tyr	Glu 120	Leu	His	Leu	Gly	Thr 125	Phe	Thr	Pro
Glu	Gly 130	Thr	Leu	Glu	Ala	Ala 135	Ala	Gly	Lys	Leu	Asp 140	Tyr	Leu	Ala	Gly
Leu 145	Gly	Val	Asp	Phe	Ile 150	Glu	Leu	Leu	Pro	Val 155	Asn	Ala	Phe	Asn	Gly 160
Thr	His	Asn	Trp	Gly 165	Tyr	Asp	Gly	Val	Gln 170	Trp	Phe	Ala	Val	His 175	Glu
Ala	Tyr	Gly	Gly 180	Pro	Glu	Ala	Tyr	Gln 185	Arg	Phe	Val	Asp	Ala 190	Ala	His
Ala	Ala	Gly 195	Leu	Gly	Val	Ile	Gln 200	Asp	Val	Val	Tyr	Asn 205	His	Leu	Gly
Pro	Ser 210	Gly	Asn	Tyr	Leu	Pro 215	Arg	Phe	Gly	Pro	Tyr 220	Leu	Lys	Gln	Gly
Glu 225	Gly	Asn	Thr	Trp	Gly 230	Asp	Ser	Val	Asn	Leu 235	Asp	Gly	Pro	Gly	Ser 240
Asp	His	Val	Arg	Arg 245	Tyr	Ile	Leu	Asp	Asn 250	Leu	Ala	Met	Trp	Leu 255	Arg
Asp	Tyr	Arg	Val 260	Asp	Gly	Leu	Arg	Leu 265	Asp	Ala	Val	His	Ala 270	Leu	Lys
Asp	Glu	Arg 275	Ala	Val	His	Ile	Leu 280	Glu	Asp	Phe	Gly	Ala 285	Leu	Ala	Asp
Gln	Ile 290	Ser	Ala	Glu	Val	Gly 295	Arg	Pro	Leu	Thr	Leu 300	Ile	Ala	Glu	Ser
Asp 305	Leu	Asn	Asn	Pro	Arg 310	Leu	Leu	Tyr	Pro	Arg 315	Asp	Val	Asn	Gly	Tyr 320
Gly	Leu	Glu	Gly	Gln 325	Trp	Ser	Asp	Asp	Phe 330	His	His	Ala	Val	His 335	Val
Asn	Val	Thr	Gly 340	Glu	Thr	Thr	Gly	Tyr 345	Tyr	Ser	Asp	Phe	Asp 350	Ser	Leu
Ala	Ala	Leu 355	Ala	Lys	Val	Leu	Arg 360	Asp	Gly	Phe	Phe	His 365	Asp	Gly	Ser
Tyr	Ser 370	Ser	Phe	Arg	Glu	Arg 375	His	His	Gly	Arg	Pro 380	Ile	Asn	Phe	Ser
Ala 385	Val	His	Pro	Ala	Ala 390	Leu	Val	Val	Cys	Ser 395	Gln	Asn	His	Asp	Gln 400
Ile	Gly	Asn	Arg	Ala 405	Thr	Gly	Asp	Arg	Leu 410	Ser	Gln	Thr	Leu	Pro 415	Tyr
Gly	Ser	Leu	Ala 420	Leu	Ala	Ala	Val	Leu 425	Thr	Leu	Thr	Gly	Pro 430	Phe	Thr
Pro	Met	Leu 435	Leu	Met	Gly	Glu	Glu 440	Tyr	Gly	Ala	Ser	Thr 445	Pro	Trp	Gln



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Pro Val Gln Gly Ala Gly Arg Phe Asp Ile Trp Ala Pro Glu Ala Gly  
1 5 10 15  
Thr Val Thr Leu Leu  
20

## ( 2 ) INFORMATION FOR SEQ ID NO:8:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 17 amino acids  
( B ) TYPE: amino acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: peptide

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asp Trp Ala Glu Ala Ser Ala Gly Asp His Ala Arg Leu Leu Glu  
1 5 10 15  
Leu

## ( 2 ) INFORMATION FOR SEQ ID NO:9:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 20 amino acids  
( B ) TYPE: amino acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: peptide

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Phe Glu Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp Pro Gln  
1 5 10 15  
Asp Pro Glu Thr  
20

## ( 2 ) INFORMATION FOR SEQ ID NO:10:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 20 amino acids  
( B ) TYPE: amino acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: peptide

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Val Leu Gly Pro Ala Arg Tyr Asp Val Trp Ala Pro Asn Ala Glu  
1 5 10 15  
Ser Val Thr Leu  
20

## ( 2 ) INFORMATION FOR SEQ ID NO:11:

( i ) SEQUENCE CHARACTERISTICS:  
( A ) LENGTH: 2161 base pairs  
( B ) TYPE: nucleic acid  
( C ) STRANDEDNESS: single  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( i x ) FEATURE:

( A ) NAME/KEY: CDS  
( B ) LOCATION: 207..1994

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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GGCGCCGGGGG GAGTGCTGGC GCTTGCCACC CGGCTCCCCT ACGGGCTGGA ACAGTCGGGC																60
GGCTGGCGGGG ACACCGCCGT CGAGCTTGAA GCCGCCATGA CGGACGAACT GACCGGCTCC																120
ACTTTCGGGC CGGGACCGGC GGCGCTGTCA GAAGTCTTCC GGGCCTACCC GGTGGCCTTG																180
TTGGTCCCCG CGACAGGAGG CAAGTC ATG ACG CAG CCC AAC GAT GCG GCC AAG																233
Met Thr Gln Pro Asn Asp Ala Ala Lys																
600 605																
CCG GTG CAG GGA GCG GGG CGC TTC GAT ATC TGG GCG CCC GAG GCA GGC																281
Pro Val Gln Gly Ala Gly Arg Phe Asp Ile Trp Ala Pro Glu Ala Gly																
610 615 620																
ACC GTA ACG CTG CTG GCC GGC GGG GAG CGC TAC GAG ATG GGC CGC CGC																329
Thr Val Thr Leu Leu Ala Gly Gly Glu Arg Tyr Glu Met																635
625 630 635																
CCC GGC AAC GGG CCG GCG GAC GAA GGC TGG TGG ACG GCC GCG GAT GCA																377
Pro Gly Asn Gly Pro Ala Asp Glu Gly Trp Trp Thr Ala Ala Asp Ala																
640 645 650																
CCG ACA GGC GCG GAC GTG GAC TAC GGA TAC CTG CTC GAC GGC GAC GAA																425
Pro Thr Gly Ala Asp Val Asp Tyr Gly Tyr Leu Leu Asp Gly Asp Glu																670
655 660 665 670																
ATC CCG CTG CCG GAC CCC CGG ACC CGC CGC CAG CCC GAA GGC GTC CAT																473
Ile Pro Leu Pro Asp Pro Arg Thr Arg Arg Gln Pro Glu Gly Val His																685
675 680 685																
GCC CTG TCC CGG ACC TTC GAC CCC GGC GCC CAC CGC TGG CAG GAC GCC																521
Ala Leu Ser Arg Thr Phe Asp Pro Gly Ala His Arg Trp Gln Asp Ala																
690 695 700																
GGG TGG CAG GGC AGG GAA CTC CAG GGC TCC GTG ATT TAC GAA CTC CAC																569
Gly Trp Gln Gly Arg Glu Leu Gln Gly Ser Val Ile Tyr Glu Leu His																
705 710 715																
ATC GGA ACG TTC ACG CCG GAA GGC ACG CTG GAC GCC GCC GCG GGC AAG																617
Ile Gly Thr Phe Thr Pro Glu Gly Thr Leu Asp Ala Ala Gly Lys																
720 725 730																
CTG GAC TAC CTC GCC GGC CTG GGC ATC GAC TTC ATT GAG CTG CTG CCC																665
Leu Asp Tyr Leu Ala Gly Leu Gly Ile Asp Phe Ile Glu Leu Leu Pro																750
735 740 745 750																
GTG AAT GCC TTC AAC GGC ACG CAC AAC TGG GGC TAC GAC GGC GTC CAG																713
Val Asn Ala Phe Asn Gly Thr His Asn Trp Gly Tyr Asp Gly Val Gln																765
755 760 765																
TGG TTT GCC GTG CAT GAA GGC TAC GGC GGG CCT GCG GCG TAC CAG CGG																761
Trp Phe Ala Val His Glu Gly Tyr Gly Gly Pro Ala Ala Tyr Gln Arg																
770 775 780																
TTC GTG GAT GCG GCC CAC GCG GCC GGC CTC GGC GTC ATC CAG GAC GTG																809
Phe Val Asp Ala Ala His Ala Ala Gly Leu Gly Val Ile Gln Asp Val																
785 790 795																
GTC TAC AAC CAC CTC GGG CCG AGC GGC AAC TAC CTC CCC AGG TAC GGC																857
Val Tyr Asn His Leu Gly Pro Ser Gly Asn Tyr Leu Pro Arg Tyr Gly																
800 805 810																
CCG TAC CTC AAG CAC GGC GAA GGC AAC ACC TGG GGC GAT TCG GTC AAC																905
Pro Tyr Leu Lys His Gly Glu Gly Asn Thr Trp Gly Asp Ser Val Asn																830
815 820 825 830																
CTG GAC GGG CCG GGA TCC GAC CAC GTC CGC CAG TAC ATC CTG GAC AAC																953
Leu Asp Gly Pro Gly Ser Asp His Val Arg Gln Tyr Ile Leu Asp Asn																845
835 840 845																
GTG GCC ATG TGG CTG CGC GAC TAC CGG GTG GAC GGC CTC CGC CTG GAC																1001
Val Ala Met Trp Leu Arg Asp Tyr Arg Val Asp Gly Leu Arg Leu Asp																
850 855 860																
GCC GTC CAC GCC CTG AAG GAT GAG CGG GCC GTC CAC ATC CTG GAG GAG																1049
Ala Val His Ala Leu Lys Asp Glu Arg Ala Val His Ile Leu Glu Glu																
865 870 875																
TTC GGC GCG CTG GCG GAC GCC CTG TCG TCC GAA GGC GGC CCG CTG																1097
Phe Gly Ala Leu Ala Asp Ala Leu Ser Ser Glu Gly Gly Arg Pro Leu																

[illegible]



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CAGGATGGAA	CGTATGACTT	TTCTGGCAGC	GGACAAACGC	TACGAAACCA	TGCCATACCG	2 1 3 4
CCGCGTCGGA	CGCAGCGGGC	TGAAGCT				2 1 6 1

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( 2 ) INFORMATION FOR SEQ ID NO:12:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 596 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Thr	Gln	Pro	Asn	Asp	Ala	Ala	Lys	Pro	Val	Gln	Gly	Ala	Gly	Arg
1				5					10					15	
Phe	Asp	Ile	Trp	Ala	Pro	Glu	Ala	Gly	Thr	Val	Thr	Leu	Leu	Ala	Gly
			20					25					30		
Gly	Glu	Arg	Tyr	Glu	Met	Gly	Arg	Arg	Pro	Gly	Asn	Gly	Pro	Ala	Asp
		35					40					45			
Glu	Gly	Trp	Trp	Thr	Ala	Ala	Asp	Ala	Pro	Thr	Gly	Ala	Asp	Val	Asp
	50					55					60				
Tyr	Gly	Tyr	Leu	Leu	Asp	Gly	Asp	Glu	Ile	Pro	Leu	Pro	Asp	Pro	Arg
65					70					75					80
Thr	Arg	Arg	Gln	Pro	Glu	Gly	Val	His	Ala	Leu	Ser	Arg	Thr	Phe	Asp
				85					90					95	
Pro	Gly	Ala	His	Arg	Trp	Gln	Asp	Ala	Gly	Trp	Gln	Gly	Arg	Glu	Leu
			100					105					110		
Gln	Gly	Ser	Val	Ile	Tyr	Glu	Leu	His	Ile	Gly	Thr	Phe	Thr	Pro	Glu
		115					120					125			
Gly	Thr	Leu	Asp	Ala	Ala	Ala	Gly	Lys	Leu	Asp	Tyr	Leu	Ala	Gly	Leu
	130					135					140				
Gly	Ile	Asp	Phe	Ile	Glu	Leu	Leu	Pro	Val	Asn	Ala	Phe	Asn	Gly	Thr
145					150					155					160
His	Asn	Trp	Gly	Tyr	Asp	Gly	Val	Gln	Trp	Phe	Ala	Val	His	Glu	Gly
				165					170					175	
Tyr	Gly	Gly	Pro	Ala	Ala	Tyr	Gln	Arg	Phe	Val	Asp	Ala	Ala	His	Ala
			180					185					190		
Ala	Gly	Leu	Gly	Val	Ile	Gln	Asp	Val	Val	Tyr	Asn	His	Leu	Gly	Pro
		195					200					205			
Ser	Gly	Asn	Tyr	Leu	Pro	Arg	Tyr	Gly	Pro	Tyr	Leu	Lys	His	Gly	Glu
	210					215					220				
Gly	Asn	Thr	Trp	Gly	Asp	Ser	Val	Asn	Leu	Asp	Gly	Pro	Gly	Ser	Asp
225					230				235					240	
His	Val	Arg	Gln	Tyr	Ile	Leu	Asp	Asn	Val	Ala	Met	Trp	Leu	Arg	Asp
				245					250					255	
Tyr	Arg	Val	Asp	Gly	Leu	Arg	Leu	Asp	Ala	Val	His	Ala	Leu	Lys	Asp
			260					265					270		
Glu	Arg	Ala	Val	His	Ile	Leu	Glu	Glu	Phe	Gly	Ala	Leu	Ala	Asp	Ala
		275					280					285			
Leu	Ser	Ser	Glu	Gly	Gly	Arg	Pro	Leu	Thr	Leu	Ile	Ala	Glu	Ser	Asp
	290					295					300				
Leu	Asn	Asn	Pro	Arg	Leu	Leu	Tyr	Pro	Arg	Asp	Val	Asn	Gly	Tyr	Gly
305					310					315					320
Leu	Ala	Gly	Gln	Trp	Ser	Asp	Asp	Phe	His	His	Ala	Val	His	Val	Asn
				325					330					335	
Val	Ser	Gly	Glu	Thr	Thr	Gly	Tyr	Tyr	Ser	Asp	Phe	Asp	Ser	Leu	Gly

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3 4 0						3 4 5						3 5 0				
Ala	Leu	Ala 3 5 5	Lys	Val	Leu	Arg	Asp 3 6 0	Gly	Phe	Phe	His	Asp 3 6 5	Gly	Ser	Tyr	
Ser	Ser 3 7 0	Phe	Arg	Gly	Arg	Cys 3 7 5	His	Gly	Arg	Pro	Ile 3 8 0	Asn	Phe	Ser	Ala	
Val 3 8 5	His	Pro	Ala	Ala	Leu 3 9 0	Val	Val	Cys	Ser	Gln 3 9 5	Asn	His	Asp	Gln	Ile 4 0 0	
Gly	Asn	Arg	Ala	Thr 4 0 5	Gly	Asp	Arg	Leu	Ser 4 1 0	Gln	Ser	Leu	Pro	Tyr 4 1 5	Gly	
Ser	Leu	Ala	Leu 4 2 0	Ala	Ala	Val	Leu	Thr 4 2 5	Leu	Thr	Gly	Pro	Phe 4 3 0	Thr	Pro	
Met	Leu	Phe 4 3 5	Met	Gly	Glu	Glu	Tyr 4 4 0	Gly	Ala	Thr	Thr	Pro 4 4 5	Trp	Gln	Phe	
Phe	Thr 4 5 0	Ser	His	Pro	Glu	Pro 4 5 5	Glu	Leu	Gly	Lys	Ala 4 6 0	Thr	Ala	Glu	Gly	
Arg 4 6 5	Ile	Arg	Glu	Phe	Glu 4 7 0	Arg	Met	Gly	Trp	Asp 4 7 5	Pro	Ala	Val	Val	Pro 4 8 0	
Asp	Pro	Gln	Asp	Pro 4 8 5	Glu	Thr	Phe	Thr	Arg 4 9 0	Ser	Lys	Leu	Asp	Trp 4 9 5	Ala	
Glu	Ala	Ser	Ala 5 0 0	Gly	Asp	His	Ala	Arg 5 0 5	Leu	Leu	Glu	Leu	Tyr 5 1 0	Arg	Ser	
Leu	Ile	Thr 5 1 5	Leu	Arg	Arg	Ser	Thr 5 2 0	Pro	Glu	Leu	Ala	Arg 5 2 5	Leu	Gly	Phe	
Ala	Asp 5 3 0	Thr	Ala	Val	Glu	Phe 5 3 5	Asp	Asp	Asp	Ala	Arg 5 4 0	Trp	Leu	Arg	Tyr	
Trp 5 4 5	Arg	Gly	Gly	Val	Gln 5 5 0	Val	Val	Leu	Asn	Phe 5 5 5	Ala	Asp	Arg	Pro	Ile 5 6 0	
Ser	Leu	Asp	Arg	Pro 5 6 5	Gly	Thr	Ala	Leu	Leu 5 7 0	Leu	Ala	Thr	Asp	Asp 5 7 5	Ala	
Val	Arg	Met	Asp 5 8 0	Gly	Val	Gln	Val	Glu 5 8 5	Leu	Pro	Pro	Leu	Ser 5 9 0	Ala	Ala	
Val	Leu	Arg 5 9 5	Asp													

( 2 ) INFORMATION FOR SEQ ID NO:13:

( i ) SEQUENCE CHARACTERISTICS:  
 ( A ) LENGTH: 2056 base pairs  
 ( B ) TYPE: nucleic acid  
 ( C ) STRANDEDNESS: single  
 ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( i x ) FEATURE:  
 ( A ) NAME/KEY: CDS  
 ( B ) LOCATION: 90..1883

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGGCTTCG	GACCGGGGGC	AGTGAAGATC	GCCGACATCT	TCCGGTCGTT	CCCCGTTGCG	6 0										
CTGCTGGTGC	CGCAGACAGG	AGGAGAGTC	ATG	ACG	CAC	ACC	TAC	CCG	CGG	GAA	11 3					
			Met	Thr	His	6 0 0										
GCC	GCG	AAA	CCC	GTC	CTG	GGC	CCC	GCA	CGC	TAC	GAC	GTC	TGG	GCG	CCC	16 1
Ala	Ala	Lys	Pro	Val	Leu	Gly	Pro	Ala	Arg	Tyr	Asp	Val	Trp	Ala	Pro	6 2 0
6 0 5					6 1 0					6 1 5						
AAC	GCT	GAA	TCC	GTG	ACG	CTG	CTG	GCC	GGC	GGG	GAG	CGC	TAC	GCC	ATG	20 9
Asn	Ala	Glu	Ser	Val	Thr	Leu	Leu	Ala	Gly	Gly	Glu	Arg	Tyr	Ala	Met	6 3 5
				6 2 5					6 3 0							

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CAG Gln	CGC Arg	CGG Arg	GCC Ala 6 4 0	GAG Glu	ACC Thr	GGG Gly	CCG Pro	GAG Glu 6 4 5	GAC Asp	GCC Ala	GGC Gly	TGG Trp 6 5 0	TGG Trp	ACC Thr	GCC Ala	2 5 7
GCC Ala	GGC Gly	GCG Ala 6 5 5	CCT Pro	ACG Thr	GAT Asp	GGC Gly	AAC Asn 6 6 0	GTG Val	GAC Asp	TAC Tyr	GGG Gly 6 6 5	TAC Tyr 6 6 5	CTT Leu	CTG Leu	GAC Asp	3 0 5
GGC Gly 6 7 0	GAC Asp	GAA Glu	ACA Thr	CCG Pro	CTT Leu	CCG Pro 6 7 5	GAT Asp	CCA Pro	CGG Arg	ACC Thr	CGC Arg 6 8 0	CGC Arg	CAG Gln	CCC Pro	GAC Asp	3 5 3
GGC Gly 6 8 5	GTC Val	CAC His	GCC Ala	CTG Leu	TCC Ser 6 9 0	CGC Arg	ACG Thr	TTC Phe	GAC Asp 6 9 5	CCG Pro	TCC Ser	GCG Ala	TAC Tyr	AGC Ser	TGG Trp 7 0 0	4 0 1
CAG Gln	GAC Asp	GAC Asp	GCC Ala	TGG Trp 7 0 5	CAG Gln	GGC Gly	AGG Arg	GAA Glu 7 1 0	CTG Leu 7 1 0	CAG Gln	GGC Gly	GCC Ala	GTC Val	ATC Ile 7 1 5	TAC Tyr	4 4 9
GAG Glu	CTC Leu	CAC His	CTC Leu 7 2 0	GGA Gly	ACA Thr	TTC Phe	ACG Thr	CCC Pro 7 2 5	GAA Glu	GGG Gly	ACG Thr	CTG Leu 7 3 0	GAG Glu 7 3 0	GCG Ala	GCC Ala	4 9 7
GCC Ala	GGA Gly	AAG Lys 7 3 5	CTG Leu	GAC Asp	TAC Tyr	CTC Leu	GCC Ala 7 4 0	GGC Gly	TTG Leu	GGC Gly	GTC Val	GAC Asp 7 4 5	TTC Phe	ATC Ile	GAG Glu	5 4 5
CTG Leu 7 5 0	CTG Leu 7 5 0	CCG Pro	GTG Val	AAC Asn	GCT Ala	TTC Phe 7 5 5	AAC Asn	GGC Gly	ACG Thr	CAC His	AAC Asn 7 6 0	TGG Trp	GGT Gly	TAC Tyr	GAC Asp	5 9 3
GGT Gly 7 6 5	GTC Val	CAG Gln	TGG Trp	TTC Phe	GCT Ala 7 7 0	GTG Val	CAC His	GAG Glu	GCA Ala	TAC Tyr 7 7 5	GGC Gly	GGG Gly	CCG Pro	GAA Glu	GCG Ala 7 8 0	6 4 1
TAC Tyr	CAG Gln	CGG Arg	TTC Phe 7 8 5	GTC Val 7 8 5	GAC Asp	GCC Ala	GCC Ala	CAC His 7 9 0	GCC Ala	GCA Ala	GGC Gly	CTT Leu	GGC Gly	GTG Val 7 9 5	ATC Ile	6 8 9
CAG Gln	GAC Asp	GTG Val 8 0 0	GTC Val 8 0 0	TAC Tyr	AAC Asn	CAC His	CTC Leu	GGC Gly 8 0 5	CCC Pro	AGC Ser	GGG Gly	AAC Asn 8 1 0	TAC Tyr 8 1 0	CTG Leu	CCG Pro	7 3 7
CGG Arg	TTC Phe	GGG Gly 8 1 5	CCG Pro	TAC Tyr	CTC Leu	AAG Lys	CAG Gln 8 2 0	GGC Gly	GAG Glu	GGT Gly	AAC Asn	ACG Thr 8 2 5	TGG Trp	GGC Gly	GAC Asp	7 8 5
TCG Ser 8 3 0	GTG Val	AAC Asn	CTG Leu	GAC Asp	GGG Gly	CCC Pro 8 3 5	GGC Gly	TCC Ser	GAC Asp	CAT His	GTG Val 8 4 0	CGC Arg	CGG Arg	TAC Tyr	ATC Ile	8 3 3
CTG Leu 8 4 5	GAC Asp	AAC Asn	CTG Leu	GCC Ala	ATG Met 8 5 0	TGG Trp	CTG Leu	CGT Arg	GAC Asp	TAC Tyr 8 5 5	CGG Arg	GTG Val	GAC Asp	GGC Gly	CTG Leu 8 6 0	8 8 1
CGG Arg	CTG Leu	GAC Asp	GCC Ala 8 6 5	GTC Val 8 6 5	CAC His	GCC Ala	CTG Leu	AAG Lys 8 7 0	GAT Asp 8 7 0	GAG Glu	CGG Arg	GCG Ala	GTG Val 8 7 5	CAC His 8 7 5	ATC Ile	9 2 9
CTG Leu	GAG Glu	GAC Asp 8 8 0	TTC Phe 8 8 0	GGG Gly	GCG Ala	CTG Leu	GCC Ala	GAT Asp 8 8 5	CAG Gln	ATC Ile	TCC Ser	GCC Ala 8 9 0	GAG Glu 8 9 0	GTG Val	GGA Gly	9 7 7
CGG Arg	CCG Pro	CTG Leu 8 9 5	ACG Thr	CTC Leu	ATC Ile	GCC Ala	GAG Glu 9 0 0	TCC Ser	GAC Asp	CTC Leu	AAC Asn 9 0 5	AAC Asn 9 0 5	CCG Pro	CGG Arg	CTG Leu	1 0 2 5
CTG Leu 9 1 0	TAC Tyr 9 1 0	CCG Pro	CGG Arg	GAC Asp	GTC Val	AAC Asn 9 1 5	GGG Gly	TAC Tyr	GGG Gly	CTG Leu	GAA Glu 9 2 0	GGG Gly	CAG Gln	TGG Trp	AGC Ser	1 0 7 3
GAC Asp 9 2 5	GAC Asp	TTC Phe	CAC His	CAC His	GCC Ala 9 3 0	GTC Val	CAC His	GTC Val	AAC Asn 9 3 5	GTC Val	ACC Thr	GGC Gly	GAA Glu	ACC Thr	ACC Thr 9 4 0	1 1 2 1
GGC Gly	TAC Tyr	TAC Tyr	AGT Ser 9 4 5	GAC Asp 9 4 5	TTC Phe	GAC Asp	TCG Ser	CTG Leu 9 5 0	GCC Ala 9 5 0	GCC Ala	CTC Leu	GCC Ala	AAG Lys	GTG Val 9 5 5	CTC Leu	1 1 6 9

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CGG	GAC	GGC	TTC	TTC	CAC	GAC	GGC	AGC	TAC	TCC	AGC	TTC	CGG	GAA	CGC	1 2 1 7
Arg	Asp	Gly	Phe	Phe	His	Asp	Gly	Ser	Tyr	Ser	Ser	Phe	Arg	Glu	Arg	
		9 6 0						9 6 5					9 7 0			
CAC	CAC	GGA	CGG	CCG	ATT	AAT	TTC	AGC	GCC	GTA	CAC	CCA	GCC	GCC	CTG	1 2 6 5
His	His	Gly	Arg	Pro	Ile	Asn	Phe	Ser	Ala	Val	His	Pro	Ala	Ala	Leu	
		9 7 5					9 8 0					9 8 5				
GTG	GTC	TGT	TCG	CAG	AAC	CAC	GAC	CAG	ATC	GGC	AAC	CGT	GCC	ACG	GGG	1 3 1 3
Val	Val	Cys	Ser	Gln	Asn	His	Asp	Gln	Ile	Gly	Asn	Arg	Ala	Thr	Gly	
	9 9 0					9 9 5					1 0 0 0					
GAC	CGG	CTC	TCC	CAG	ACC	CTG	CCG	TAC	GGA	AGC	CTG	GCC	CTC	GCT	GCG	1 3 6 1
Asp	Arg	Leu	Ser	Gln	Thr	Leu	Pro	Tyr	Gly	Ser	Leu	Ala	Leu	Ala	Ala	
1 0 0 5				1 0 1 0						1 0 1 5					1 0 2 0	
GTG	CTG	ACC	CTG	ACG	GGA	CCC	TTC	ACG	CCC	ATG	CTG	CTC	ATG	GGC	GAG	1 4 0 9
Val	Leu	Thr	Leu	Thr	Gly	Pro	Phe	Thr	Pro	Met	Leu	Leu	Met	Gly	Glu	
				1 0 2 5					1 0 3 0					1 0 3 5		
GAG	TAC	GGC	GCC	AGC	ACG	CCG	TGG	CAG	TTT	TTC	ACC	TCG	CAC	CCG	GAG	1 4 5 7
Glu	Tyr	Gly	Ala	Ser	Thr	Pro	Trp	Gln	Phe	Phe	Thr	Ser	His	Pro	Glu	
			1 0 4 0					1 0 4 5					1 0 5 0			
CCG	GAG	CTC	GGC	AAG	GCC	ACC	GCG	GAG	GGC	CGG	ATC	AAG	GAG	TTC	GAG	1 5 0 5
Pro	Glu	Leu	Gly	Lys	Ala	Thr	Ala	Glu	Gly	Arg	Ile	Lys	Glu	Phe	Glu	
		1 0 5 5					1 0 6 0					1 0 6 5				
CGC	ATG	GGG	TGG	GAT	CCC	GCC	GTC	GTG	CCC	GAT	CCC	CAG	GAT	CCT	GAG	1 5 5 3
Arg	Met	Gly	Trp	Asp	Pro	Ala	Val	Val	Pro	Asp	Pro	Gln	Asp	Pro	Glu	
	1 0 7 0					1 0 7 5					1 0 8 0					
ACG	TTC	CGC	CGG	TCC	AAG	CTG	GAC	TGG	GCG	GAA	GCC	GCC	GAA	GGC	GAC	1 6 0 1
Thr	Phe	Arg	Arg	Ser	Lys	Leu	Asp	Trp	Ala	Glu	Ala	Ala	Glu	Gly	Asp	
1 0 8 5					1 0 9 0					1 0 9 5					1 1 0 0	
CAT	GCC	CGG	CTG	CTG	GAG	CTG	TAC	CGT	TCG	CTC	ACC	GCC	CTG	CGC	CGC	1 6 4 9
His	Ala	Arg	Leu	Leu	Glu	Leu	Tyr	Arg	Ser	Leu	Thr	Ala	Leu	Arg	Arg	
				1 1 0 5					1 1 1 0					1 1 1 5		
TCC	ACG	CCG	GAC	CTC	ACC	AAG	CTG	GGC	TTC	GAG	GAC	ACG	CAG	GTG	GCG	1 6 9 7
Ser	Thr	Pro	Asp	Leu	Thr	Lys	Leu	Gly	Phe	Glu	Asp	Thr	Gln	Val	Ala	
			1 1 2 0					1 1 2 5					1 1 3 0			
TTC	GAC	GAG	GAC	GCC	CGC	TGG	CTG	CGG	TTC	CGC	CGG	GGT	GGC	GTG	CAG	1 7 4 5
Phe	Asp	Glu	Asp	Ala	Arg	Trp	Leu	Arg	Phe	Arg	Arg	Gly	Gly	Val	Gln	
		1 1 3 5					1 1 4 0					1 1 4 5				
GTG	CTG	CTC	AAC	TTC	TCG	GAA	CAG	CCC	GTG	AGC	CTG	GAC	GGG	GCG	GGC	1 7 9 3
Val	Leu	Leu	Asn	Phe	Ser	Glu	Gln	Pro	Val	Ser	Leu	Asp	Gly	Ala	Gly	
	1 1 5 0					1 1 5 5					1 1 6 0					
ACG	GCC	CTG	CTG	CTG	GCC	ACC	GAC	GAC	GCC	GTC	CGG	CTA	GAA	GGT	GAG	1 8 4 1
Thr	Ala	Leu	Leu	Leu	Ala	Thr	Asp	Asp	Ala	Val	Arg	Leu	Glu	Gly	Glu	
1 1 6 5					1 1 7 0					1 1 7 5					1 1 8 0	
CGT	GCG	GAA	CTC	GGT	CCG	CTG	AGC	GCC	GCC	GTC	GTC	AGC	GAC			1 8 8 3
Arg	Ala	Glu	Leu	Gly	Pro	Leu	Ser	Ala	Ala	Val	Val	Ser	Asp			
				1 1 8 5					1 1 9 0							
TGACGTTTTTC	TTGGGGGGCGG	CGTCCACCGC	CGGTGACCGG	ATGGTGGACG	TCCGCCCCGA											1 9 4 3
AGCCTCGGCG	CGGCTGGCAG	GATGGAACGC	ATGACTTATG	TGGCCTCGGA	CACCCGCTAC											2 0 0 3
GACACCATGC	CCTACCGCCG	CGTCGGACGC	AGCGGCCTCA	AACTGCCGGC	CAT											2 0 5 6

( 2 ) INFORMATION FOR SEQ ID NO:14:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 598 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Thr His Thr Tyr Pro Arg Glu Ala Ala Lys Pro Val Leu Gly Pro

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1			5					10					15				
Ala	Arg	Tyr	Asp <sub>20</sub>	Val	Trp	Ala	Pro	Asn <sub>25</sub>	Ala	Glu	Ser	Val	Thr <sub>30</sub>	Leu	Leu		
Ala	Gly	Gly <sub>35</sub>	Glu	Arg	Tyr	Ala	Met <sub>40</sub>	Gln	Arg	Arg	Ala	Glu <sub>45</sub>	Thr	Gly	Pro		
Glu	Asp <sub>50</sub>	Ala	Gly	Trp	Trp	Thr <sub>55</sub>	Ala	Ala	Gly	Ala	Pro <sub>60</sub>	Thr	Asp	Gly	Asn		
Val <sub>65</sub>	Asp	Tyr	Gly	Tyr	Leu <sub>70</sub>	Leu	Asp	Gly	Asp	Glu <sub>75</sub>	Thr	Pro	Leu	Pro	Asp <sub>80</sub>		
Pro	Arg	Thr	Arg	Arg <sub>85</sub>	Gln	Pro	Asp	Gly	Val <sub>90</sub>	His	Ala	Leu	Ser	Arg <sub>95</sub>	Thr		
Phe	Asp	Pro	Ser <sub>100</sub>	Ala	Tyr	Ser	Trp	Gln <sub>105</sub>	Asp	Asp	Ala	Trp	Gln <sub>110</sub>	Gly	Arg		
Glu	Leu	Gln <sub>115</sub>	Gly	Ala	Val	Ile	Tyr <sub>120</sub>	Glu	Leu	His	Leu	Gly <sub>125</sub>	Thr	Phe	Thr		
Pro	Glu <sub>130</sub>	Gly	Thr	Leu	Glu	Ala <sub>135</sub>	Ala	Ala	Gly	Lys	Leu <sub>140</sub>	Asp	Tyr	Leu	Ala		
Gly <sub>145</sub>	Leu	Gly	Val	Asp	Phe <sub>150</sub>	Ile	Glu	Leu	Leu	Pro <sub>155</sub>	Val	Asn	Ala	Phe	Asn <sub>160</sub>		
Gly	Thr	His	Asn	Trp <sub>165</sub>	Gly	Tyr	Asp	Gly	Val <sub>170</sub>	Gln	Trp	Phe	Ala	Val <sub>175</sub>	His		
Glu	Ala	Tyr	Gly <sub>180</sub>	Gly	Pro	Glu	Ala	Tyr <sub>185</sub>	Gln	Arg	Phe	Val	Asp <sub>190</sub>	Ala	Ala		
His	Ala	Ala <sub>195</sub>	Gly	Leu	Gly	Val	Ile <sub>200</sub>	Gln	Asp	Val	Val	Tyr <sub>205</sub>	Asn	His	Leu		
Gly	Pro <sub>210</sub>	Ser	Gly	Asn	Tyr	Leu <sub>215</sub>	Pro	Arg	Phe	Gly	Pro <sub>220</sub>	Tyr	Leu	Lys	Gln		
Gly <sub>225</sub>	Glu	Gly	Asn	Thr	Trp <sub>230</sub>	Gly	Asp	Ser	Val	Asn <sub>235</sub>	Leu	Asp	Gly	Pro	Gly <sub>240</sub>		
Ser	Asp	His	Val	Arg <sub>245</sub>	Arg	Tyr	Ile	Leu	Asp <sub>250</sub>	Asn	Leu	Ala	Met	Trp <sub>255</sub>	Leu		
Arg	Asp	Tyr	Arg <sub>260</sub>	Val	Asp	Gly	Leu	Arg <sub>265</sub>	Leu	Asp	Ala	Val	His <sub>270</sub>	Ala	Leu		
Lys	Asp	Glu <sub>275</sub>	Arg	Ala	Val	His	Ile <sub>280</sub>	Leu	Glu	Asp	Phe	Gly <sub>285</sub>	Ala	Leu	Ala		
Asp	Gln <sub>290</sub>	Ile	Ser	Ala	Glu	Val <sub>295</sub>	Gly	Arg	Pro	Leu	Thr <sub>300</sub>	Leu	Ile	Ala	Glu		
Ser <sub>305</sub>	Asp	Leu	Asn	Asn	Pro <sub>310</sub>	Arg	Leu	Leu	Tyr	Pro <sub>315</sub>	Arg	Asp	Val	Asn	Gly <sub>320</sub>		
Tyr	Gly	Leu	Glu	Gly <sub>325</sub>	Gln	Trp	Ser	Asp	Asp <sub>330</sub>	Phe	His	His	Ala	Val <sub>335</sub>	His		
Val	Asn	Val	Thr <sub>340</sub>	Gly	Glu	Thr	Thr	Gly <sub>345</sub>	Tyr	Tyr	Ser	Asp	Phe <sub>350</sub>	Asp	Ser		
Leu	Ala	Ala <sub>355</sub>	Leu	Ala	Lys	Val	Leu <sub>360</sub>	Arg	Asp	Gly	Phe	Phe <sub>365</sub>	His	Asp	Gly		
Ser	Tyr <sub>370</sub>	Ser	Ser	Phe	Arg	Glu <sub>375</sub>	Arg	His	His	Gly	Arg <sub>380</sub>	Pro	Ile	Asn	Phe		
Ser <sub>385</sub>	Ala	Val	His	Pro	Ala <sub>390</sub>	Ala	Leu	Val	Val	Cys <sub>395</sub>	Ser	Gln	Asn	His	Asp <sub>400</sub>		
Gln	Ile	Gly	Asn	Arg <sub>405</sub>	Ala	Thr	Gly	Asp	Arg <sub>410</sub>	Leu	Ser	Gln	Thr	Leu <sub>415</sub>	Pro		
Tyr	Gly	Ser	Leu <sub>420</sub>	Ala	Leu	Ala	Ala	Val <sub>425</sub>	Leu	Thr	Leu	Thr	Gly <sub>430</sub>	Pro	Phe		

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Thr	Pro	Met	Leu	Leu	Met	Gly	Glu	Glu	Tyr	Gly	Ala	Ser	Thr	Pro	Trp
		435					440					445			
Gln	Phe	Phe	Thr	Ser	His	Pro	Glu	Pro	Glu	Leu	Gly	Lys	Ala	Thr	Ala
	450					455					460				
Glu	Gly	Arg	Ile	Lys	Glu	Phe	Glu	Arg	Met	Gly	Trp	Asp	Pro	Ala	Val
465					470					475					480
Val	Pro	Asp	Pro	Gln	Asp	Pro	Glu	Thr	Phe	Arg	Arg	Ser	Lys	Leu	Asp
				485					490					495	
Trp	Ala	Glu	Ala	Ala	Glu	Gly	Asp	His	Ala	Arg	Leu	Leu	Glu	Leu	Tyr
			500					505					510		
Arg	Ser	Leu	Thr	Ala	Leu	Arg	Arg	Ser	Thr	Pro	Asp	Leu	Thr	Lys	Leu
		515					520					525			
Gly	Phe	Glu	Asp	Thr	Gln	Val	Ala	Phe	Asp	Glu	Asp	Ala	Arg	Trp	Leu
	530					535					540				
Arg	Phe	Arg	Arg	Gly	Gly	Val	Gln	Val	Leu	Leu	Asn	Phe	Ser	Glu	Gln
545					550					555					560
Pro	Val	Ser	Leu	Asp	Gly	Ala	Gly	Thr	Ala	Leu	Leu	Leu	Ala	Thr	Asp
				565				570						575	
Asp	Ala	Val	Arg	Leu	Glu	Gly	Glu	Arg	Ala	Glu	Leu	Gly	Pro	Leu	Ser
			580					585					590		
Ala	Ala	Val	Val	Ser	Asp										
			595												

( 2 ) INFORMATION FOR SEQ ID NO:15:

- ( i ) SEQUENCE CHARACTERISTICS:
  - ( A ) LENGTH: 17 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: single
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTYGAYATHT GGGCNCC

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( 2 ) INFORMATION FOR SEQ ID NO:16:

- ( i ) SEQUENCE CHARACTERISTICS:
  - ( A ) LENGTH: 17 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: single
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTAACGAC GGCCAGT

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( 2 ) INFORMATION FOR SEQ ID NO:17:

- ( i ) SEQUENCE CHARACTERISTICS:
  - ( A ) LENGTH: 17 base pairs
  - ( B ) TYPE: nucleic acid
  - ( C ) STRANDEDNESS: single
  - ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGGNTGGG AYCCNGC

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( 2 ) INFORMATION FOR SEQ ID NO:18:

( i ) SEQUENCE CHARACTERISTICS:  
    ( A ) LENGTH: 14 base pairs  
    ( B ) TYPE: nucleic acid  
    ( C ) STRANDEDNESS: single  
    ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO:18:

T A Y G A Y G T N T   G G G C

1 4

We claim:

1. A method for converting a non-reducing saccharide, comprising the step of:

introducing a recombinant DNA carrying a self-replicable vector and a nucleotide sequence coding for the expression of a variant of an enzyme of SEQ ID NO: 2 or SEQ ID NO: 4, which variant acts on a non-reducing saccharide having a trehalose structure as an end unit and having a degree of glucose polymerization of 3 or higher to release trehalose, into a host microorganism to obtain a recombinant microorganism, wherein the variant has an amino acid sequence of SEQ ID NO: 2 or SEQ ID NO: 4 with one or more amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4 deleted, replaced with different amino acids, or supplemented with one or more amino acids without substantially altering the activity of the enzyme of SEQ ID NO: 2 or SEQ ID NO: 4;

culturing said recombinant microorganism having said recombinant DNA for expression of said variant enzyme in a nutrient culture medium to accumulate said variant enzyme;

recovering said accumulated variant enzyme; and

subjecting said non-reducing saccharine to the action of said recovered variant enzyme possessing trehalose releasing activity to convert said non-reducing saccharide.

2. The method according to claim 1, wherein said non-reducing saccharide is prepared by successively treating an

15 amylaceous substance selected from the group consisting of starch, amylopectin, amylose, and mixtures thereof, with acid in combination with or without amylase.

3. The method according to claim 1, wherein said non-reducing saccharide is selected from the group consisting of  $\alpha$ -glucosyltrehalose,  $\alpha$ -maltosyltrehalose,  $\alpha$ -maltotriosyltrehalose,  $\alpha$ -maltotetraosyltrehalose,  $\alpha$ -maltopentaosyltrehalose, and mixtures thereof.

4. The method according to claim 1, wherein said non-reducing saccharide has a concentration of 50 w/v % or lower in solution, and said subjecting step is carried out at a temperature of about 40°–55° C. and a pH in a range of about 6–8.

5. The method according to claim 1, wherein the variant has one or more amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4 replaced with different amino acids without substantially altering the activity of the enzyme of SEQ ID NO: 2 or SEQ ID NO: 4.

6. The method according to claim 1, wherein the variant has one or more amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4 deleted without substantially altering the activity of the enzyme of SEQ ID NO: 2 or SEQ ID NO: 4.

7. The method according to claim 1, wherein the variant has one or more amino acid residues in SEQ ID NO: 2 or SEQ ID NO: 4 supplemented with one or more amino acids without substantially altering the activity of the enzyme of SEQ ID NO: 2 or SEQ ID NO: 4.

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